

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 27, 2004, 18:12:11 ; Search time 15.9 Seconds  
(without alignments)  
29.197 Million cell updates/sec

Title: US-09-846-033B-74  
Perfect score: 7  
Sequence: 1 RSDNLQR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-716-637-30
					Sequence 30, Appl

ALIGNMENTS

RESULT 1  
US-09-716-637-30  
; Sequence 30, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: VEGF-II P2  
US-09-716-637-30

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDNLQR 7  
| | | | |  
Db 1 RSDNLQR 7

Search completed: December 27, 2004, 19:21:24  
Job time : 16.9 secs

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OM protein - protein search, using sw model  
Run on: December 27, 2004, 18:12:11 ; Search time 15.9 Seconds  
(without alignments)  
29.197 Million cell updates/sec

Title: US-09-846-033B-73  
Perfect score: 7  
Sequence: 1 RSSNLQR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0  
Searched: 478139 seqs, 66318000 residues

Word size : 7  
Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
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3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	4 US-09-716-637-28	Sequence 28, Appl
2	7	100.0	99	4 US-09-229-037-15	Sequence 15, Appl
3	7	100.0	99	4 US-09-229-037-17	Sequence 17, Appl
4	7	100.0	99	4 US-09-478-681-15	Sequence 15, Appl
5	7	100.0	99	4 US-09-478-681-17	Sequence 17, Appl
6	7	100.0	99	4 US-09-779-233-3	Sequence 3, Appl
7	7	100.0	99	4 US-09-779-233-5	Sequence 5, Appl
8	7	100.0	196	4 US-09-229-037-30	Sequence 30, Appl
9	7	100.0	196	4 US-09-478-681-30	Sequence 30, Appl
10	7	100.0	196	4 US-09-779-233-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1  
US-09-716-637-28  
; Sequence 28, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020

RESULT 2  
US-09-229-037-15  
; Sequence 15, Application US/09229037A  
; Patent No. 6534261  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George No. 6534261bert  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric Edward  
; APPLICANT: Spratt, Sharon Kaye  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using  
; TITLE OF INVENTION: Zinc Finger Proteins  
; FILE REFERENCE: 019496-002200US  
; CURRENT APPLICATION NUMBER: US/09/229,037A

RESULT 3  
US-09-229-037-17  
; Sequence 17, Application US/09229037A  
; Patent No. 6534261  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George No. 6534261bert  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric Edward  
; APPLICANT: Spratt, Sharon Kaye  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using  
; TITLE OF INVENTION: Zinc Finger Proteins  
; FILE REFERENCE: 019496-002200US  
; CURRENT APPLICATION NUMBER: US/09/229,037A

; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F2  
US-09-716-637-28

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSNLQR 7  
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Db 1 RSSNLQR 7

RESULT 2

US-09-229-037-15  
; Sequence 15, Application US/09229037A  
; Patent No. 6534261  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George No. 6534261bert  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric Edward  
; APPLICANT: Spratt, Sharon Kaye  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using  
; TITLE OF INVENTION: Zinc Finger Proteins  
; FILE REFERENCE: 019496-002200US  
; CURRENT APPLICATION NUMBER: US/09/229,037A  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 99  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP  
; OTHER INFORMATION: Construct targeting upstream 9-base pair target  
; OTHER INFORMATION: site in VEGF promoter  
US-09-229-037-15

Query Match 100.0%; Score 7; DB 4; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSNLQR 7  
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Db 53 RSSNLQR 59

RESULT 3

US-09-229-037-17  
; Sequence 17, Application US/09229037A  
; Patent No. 6534261  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George No. 6534261bert  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric Edward  
; APPLICANT: Spratt, Sharon Kaye  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using  
; TITLE OF INVENTION: Zinc Finger Proteins  
; FILE REFERENCE: 019496-002200US  
; CURRENT APPLICATION NUMBER: US/09/229,037A

; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 99  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:VEGF3a ZFP  
; OTHER INFORMATION: construct targeting downstream 9-base pair target  
; OTHER INFORMATION: site in VEGF promoter  
US-09-229-037-17

Query Match 100.0%; Score 7; DB 4; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;

QY 1 RSSNLQR 7  
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Db 53 RSSNLQR 59

RESULT 4  
US-09-478-681-15  
; Sequence 15, Application US/09478681  
; Patent No. 6607882  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 99  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP  
; OTHER INFORMATION: construct targeting upstream 9-base pair target  
; OTHER INFORMATION: site in VEGF promoter  
US-09-478-681-15

Query Match 100.0%; Score 7; DB 4; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;

QY 1 RSSNLQR 7  
|||||  
Db 53 RSSNLQR 59

RESULT 5  
US-09-478-681-17  
; Sequence 17, Application US/09478681  
; Patent No. 6607882  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06

; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 99  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:VEGF3a ZFP  
; OTHER INFORMATION: construct targeting downstream 9-base pair target  
; OTHER INFORMATION: site in VEGF promoter  
US-09-478-681-17

Query Match 100.0%; Score 7; DB 4; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;

QY 1 RSSNLQR 7  
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Db 53 RSSNLQR 59

RESULT 6  
US-09-779-233-3  
; Sequence 3, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 99  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGFP1  
US-09-779-233-3

Query Match 100.0%; Score 7; DB 4; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;

QY 1 RSSNLQR 7  
|||||  
Db 53 RSSNLQR 59

RESULT 7  
US-09-779-233-5  
; Sequence 5, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 99  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF3a  
US-09-779-233-5

Query Match 100.0%; Score 7; DB 4; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;



QY 1 RSSNLQR 7  
Db 53 RSSNLQR 59

RESULT 8  
US-09-229-037-30  
; Sequence 30, Application US/09229037A  
; Patent No. 6534261  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George No. 6534261bert  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric Edward  
; APPLICANT: Spratt, Sharon Kaye  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using  
; TITLE OF INVENTION: Zinc Finger Proteins  
; FILE REFERENCE: 019496-002200US  
; CURRENT APPLICATION NUMBER: US/09/229,037A  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:designed  
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpni to BamHI  
US-09-229-037-30

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSNLQR 7  
Db 53 RSSNLQR 59

RESULT 9  
US-09-478-681-30  
; Sequence 30, Application US/09478681  
; Patent No. 6607882  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:designed  
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpni to BamHI  
US-09-478-681-30

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSNLQR 7

Db 53 RSSNLQR 59

RESULT 10  
US-09-779-233-18  
; Sequence 18, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1  
US-09-779-233-18

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSNLQR 7  
Db 53 RSSNLQR 59

Search completed: December 27, 2004, 19:21:23  
Job time : 15.9 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 18:12:11 ; Search time 15.9 Seconds  
(without alignments)  
29.197 Million cell updates/sec

Title: US-09-846-033B-72  
Perfect score: 7  
Sequence: 1 RSSNLQR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 10

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfilese1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	7	100.0	99	4	US-09-229-037-15
3	7	100.0	99	4	US-09-229-037-17
4	7	100.0	99	4	US-09-478-681-15
5	7	100.0	99	4	US-09-478-681-17
6	7	100.0	99	4	US-09-779-233-3
7	7	100.0	99	4	US-09-779-233-5
8	7	100.0	196	4	US-09-229-037-30
9	7	100.0	196	4	US-09-478-681-30
10	7	100.0	196	4	US-09-779-233-18

ALIGNMENTS

RESULT 1  
US-09-716-637-28  
; Sequence 28, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020

; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-1 F2  
US-09-716-637-28

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSNLQR 7  
Db 1 RSSNLQR 7

RESULT 2

US-09-229-037-15  
; Sequence 15, Application US/09229037A  
; Patent No. 6534261  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George No. 6534261bert  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric Edward  
; APPLICANT: Spratt, Sharon Kaye  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using  
; TITLE OF INVENTION: Zinc Finger Proteins  
; FILE REFERENCE: 019496-002200US  
; CURRENT APPLICATION NUMBER: US/09/229,037A  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 99  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP  
; OTHER INFORMATION: construct targeting upstream 9-base pair target  
; OTHER INFORMATION: site in VEGF promoter  
US-09-229-037-15

Query Match 100.0%; Score 7; DB 4; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSNLQR 7  
Db 53 RSSNLQR 59

RESULT 3

US-09-229-037-17  
; Sequence 17, Application US/09229037A  
; Patent No. 6534261  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George No. 6534261bert  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric Edward  
; APPLICANT: Spratt, Sharon Kaye  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using  
; TITLE OF INVENTION: Zinc Finger Proteins  
; FILE REFERENCE: 019496-002200US  
; CURRENT APPLICATION NUMBER: US/09/229,037A

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; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:VEGF3a ZFP
; OTHER INFORMATION: construct targeting downstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-229-037-17

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSNLQR 7
Db 53 RSSNLQR 59

RESULT 4
US-09-478-681-15
; Sequence 15, Application US/09478681
; Patent No. 6607882
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric E.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; FILE REFERENCE: 8325-0002.10 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/478,681
; CURRENT FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP
; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-478-681-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSNLQR 7
Db 53 RSSNLQR 59

RESULT 5
US-09-478-681-17
; Sequence 17, Application US/09478681
; Patent No. 6607882
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric E.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; FILE REFERENCE: 8325-0002.10 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/478,681
; CURRENT FILING DATE: 2000-01-06
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; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:VEGF3a ZFP
; OTHER INFORMATION: construct targeting downstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-478-681-17

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSNLQR 7
Db 53 RSSNLQR 59

RESULT 6
US-09-779-233-3
; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSNLQR 7
Db 53 RSSNLQR 59

RESULT 7
US-09-779-233-5
; Sequence 5, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF3a
US-09-779-233-5

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RSSNLQR 7  
Db 53 RSSNLQR 59

## RESULT 8

US-09-229-037-30  
; Sequence 30, Application US/09229037A  
; Patent No. 6534261  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George No. 6534261bert  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric Edward  
; APPLICANT: Spratt, Sharon Kaye  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using  
; TITLE OF INVENTION: Zinc Finger Proteins  
; FILE REFERENCE: 019496-002200US  
; CURRENT APPLICATION NUMBER: US/09/229,037A  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:designed  
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpni to BamHI  
US-09-229-037-30

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSNLQR 7  
Db 53 RSSNLQR 59

## RESULT 9

US-09-478-681-30  
; Sequence 30, Application US/09478681  
; Patent No. 6607882  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:designed  
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpni to BamHI  
US-09-478-681-30

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSNLQR 7

Db 53 RSSNLQR 59

## RESULT 10

US-09-779-233-18  
; Sequence 18, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1  
US-09-779-233-18

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSNLQR 7  
Db 53 RSSNLQR 59

Search completed: December 27, 2004, 19:21:23  
Job time : 15.9 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 18:12:11 ; Search time 15.9 Seconds  
(without alignments)  
29.197 Million cell updates/sec

Title: US-09-846-033B-71  
Perfect score: 7  
Sequence: 1 RSDHLTR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
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4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	3 US-09-173-941-69	Sequence 69, Appl
2	7	100.0	7	4 US-09-494-190-69	Sequence 69, Appl
3	7	100.0	21	4 US-09-229-007A-94	Sequence 94, Appl
4	7	100.0	21	4 US-10-113-424-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1  
US-09-173-941-69  
; Sequence 69, Application US/09173941  
; Patent No. 6140081  
; GENERAL INFORMATION:  
; APPLICANT: BARBAS, Carlos F.  
; TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN  
; FILE REFERENCE: NOV00BIS  
; CURRENT APPLICATION NUMBER: US/09/173,941  
; CURRENT FILING DATE: 1998-10-16  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 69  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide

; OTHER INFORMATION: codon binding sequence  
US-09-173-941-69

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Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTR 7  
Db 1 RSDHLTR 7

RESULT 2

US-09-494-190-69  
; Sequence 69, Application US/09494190  
; Patent No. 6610512  
; GENERAL INFORMATION:  
; APPLICANT: BARBAS, Carlos F.  
; TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN  
; FILE REFERENCE: TSRI 645.2  
; CURRENT APPLICATION NUMBER: US/09/494,190  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: EP/99/07742  
; PRIOR FILING DATE: 1999-10-14  
; PRIOR APPLICATION NUMBER: US 09/173,941  
; PRIOR FILING DATE: 1998-10-16  
; NUMBER OF SEQ ID NOS: 126  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 69  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:phage display  
; OTHER INFORMATION: selected and mutagenized  
US-09-494-190-69

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTR 7  
Db 1 RSDHLTR 7

RESULT 3

US-09-229-007A-94  
; Sequence 94, Application US/09229007A  
; Patent No. 6453242  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Case, Casey C.  
; APPLICANT: Cox III, George N.  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger  
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins  
; TITLE OF INVENTION: to Bind to Preselected Sites  
; FILE REFERENCE: 019496-001800US  
; CURRENT APPLICATION NUMBER: US/09/229,007A  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 94  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence  
; OTHER INFORMATION: (F1, F2 and F3) from SBS design GR-223  
US-09-229-007A-94

Query Match 100.0%; Score 7; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTR 7  
Db 8 RSDHLTR 14

RESULT 4  
US-10-113-424-94  
; Sequence 94, Application US/10113424  
; Patent No. 6785613  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Case, Casey C.  
; APPLICANT: Cox III, George N.  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger  
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins  
; TITLE OF INVENTION: to Bind to Preslected Sites  
; FILE REFERENCE: 019496-001800US  
; CURRENT APPLICATION NUMBER: US/10/113,424  
; CURRENT FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US/09/229,007A  
; PRIOR FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 94  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP sequence  
; OTHER INFORMATION: (F1, F2 and F3) from SBS design GR-223  
US-10-113-424-94

Query Match 100.0%; Score 7; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTR 7  
Db 8 RSDHLTR 14

Search completed: December 27, 2004, 19:21:23  
Job time : 15.9 secs



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OM protein - protein search, using sw model

Run on: December 27, 2004, 18:12:11 ; Search time 15.9 Seconds  
(without alignments)  
29.197 Million cell updates/sec

Title: US-09-846-033B-70  
Perfect score: 7  
Sequence: 1 QSGNLR 7

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Gapop 60.0 , Gapext 60.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-21
					Sequence 21, Appl

ALIGNMENTS

RESULT 1  
US-09-731-558-21  
; Sequence 21, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558  
; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 7  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:SBS10  
; OTHER INFORMATION: recognition helix  
US-09-731-558-21

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGNLR 7  
Db 1 QSGNLR 7

Search completed: December 27, 2004, 19:21:23  
Job time : 16.9 secs

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OM protein - protein search, using sw model

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29.197 Million cell updates/sec

Title: US-09-846-033b-69  
Perfect score: 7  
Sequence: 1 QSGNLR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-21 Sequence 21, Appl

ALIGNMENTS

RESULT 1  
US-09-731-558-21  
; Sequence 21, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebat, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558  
; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 7  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:SSS10  
; OTHER INFORMATION: recognition helix  
US-09-731-558-21

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05; Indels 0;  
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY 1 QSGNLR 7  
| | | | |  
Db 1 QSGNLR 7

Search completed: December 27, 2004, 19:21:22  
Job time : 15.9 secs

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OM protein - protein search, using sw model

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(without alignments)  
29.197 Million cell updates/sec

Title: US-09-846-033B-68  
Perfect score: 7  
Sequence: 1 RSDHLSR 7

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Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 9

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4 US-09-731-558-14	Sequence 14, Appl
2	7	100.0	7	4 US-09-779-233-44	Sequence 44, Appl
3	7	100.0	7	4 US-09-716-637-29	Sequence 29, Appl
4	7	100.0	99	4 US-09-229-037-15	Sequence 15, Appl
5	7	100.0	99	4 US-09-478-681-15	Sequence 15, Appl
6	7	100.0	99	4 US-09-779-233-3	Sequence 3, Appl
7	7	100.0	196	4 US-09-229-037-30	Sequence 30, Appl
8	7	100.0	196	4 US-09-478-681-30	Sequence 30, Appl
9	7	100.0	196	4 US-09-779-233-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1  
US-09-731-558-14  
; Sequence 14, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731.558

; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SRS3  
; OTHER INFORMATION: recognition helix  
US-09-731-558-14

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
|||||  
Db 1 RSDHLSR 7

RESULT 2

US-09-779-233-44  
; Sequence 44, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
; OTHER INFORMATION: helix  
US-09-779-233-44

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
|||||  
Db 1 RSDHLSR 7

RESULT 3

US-09-716-637-29  
; Sequence 29, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29

Query Match      100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
   |||||
Db 1 RSDHLSR 7

RESULT 4
US-09-229-037-15
; Sequence 15, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-229-037-15

Query Match      100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
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Db 81 RSDHLSR 87

RESULT 5
US-09-478-681-15
; Sequence 15, Application US/09478681
; Patent No. 6607882
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric E.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS
; FILE REFERENCE: 8325-0002.10 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/478,681
; CURRENT FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
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; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-478-681-15

Query Match      100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
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Db 81 RSDHLSR 87

RESULT 6
US-09-779-233-3
; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3

Query Match      100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
   |||||
Db 81 RSDHLSR 87

RESULT 7
US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-229-037-30

Query Match      100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Tue Dec 28 09:45:42 2004

Qy 1 RSDHLSR 7  
 Db 178 RSDHLSR 184

RESULT 8  
 US-09-478-681-30  
 ; Sequence 30, Application US/09478681  
 ; Patent No. 6607882  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cox III, George N.  
 ; APPLICANT: Case, Casey Christopher  
 ; APPLICANT: Eisenberg, Stephen P.  
 ; APPLICANT: Jarvis, Eric E.  
 ; APPLICANT: Spratt, Sharon K.  
 ; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
 ; TITLE OF INVENTION: USING ZINC FINGER PROTEINS  
 ; FILE REFERENCE: 8325-0002.10 / S2-US3  
 ; CURRENT APPLICATION NUMBER: US/09/478,681  
 ; CURRENT FILING DATE: 2000-01-06  
 ; NUMBER OF SEQ ID NOS: 43  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 30  
 ; LENGTH: 196  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:designed  
 ; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpnl to BamHI  
 US-09-478-681-30

Query Match 100.0%; Score 7; DB 4; Length 196;  
 Best Local Similarity 100.0%; Pred. No. 0.3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSR 7  
 Db 178 RSDHLSR 184

RESULT 9  
 US-09-779-233-18  
 ; Sequence 18, Application US/09779233  
 ; Patent No. 6689558  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Case, Casey  
 ; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
 ; FILE REFERENCE: 8325-0010  
 ; CURRENT APPLICATION NUMBER: US/09/779,233  
 ; CURRENT FILING DATE: 2001-02-08  
 ; NUMBER OF SEQ ID NOS: 45  
 ; SOFTWARE: PatentIn Ver. 2.0  
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 ; LENGTH: 196  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1  
 US-09-779-233-18

Query Match 100.0%; Score 7; DB 4; Length 196;  
 Best Local Similarity 100.0%; Pred. No. 0.3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSR 7  
 Db 178 RSDHLSR 184

Search completed: December 27, 2004, 19:21:22  
 Job time : 15.9 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 18:12:11 ; Search time 15.9 Seconds  
(without alignments)  
29.197 Million cell updates/sec

Title: US-09-846-033B-57  
Perfect score: 7  
Sequence: 1 QSGSLTR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-16
					Sequence 16, App1

ALIGNMENTS

RESULT 1  
US-09-731-558-16  
; Sequence 16, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; FILE REFERENCE: 019496-003210US  
; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US/09/731,558  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 7  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:SBS5  
; OTHER INFORMATION: recognition helix  
US-09-731-558-16

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSGSLTR 7  
Db 1 QSGSLTR 7

Search completed: December 27, 2004, 19:21:22  
Job time : 15.9 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

QM protein - protein search, using sw model

Run on: December 27, 2004, 18:12:11 ; Search time 15.9 Seconds  
(without alignments)  
29.197 Million cell updates/sec

Title: US-09-846-033B-56

Perfect score: 7  
Sequence: 1 DRSNLTR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4 US-09-731-558-20	Sequence 20, Appl
2	7	100.0	27	4 US-09-424-487B-11	Sequence 11, Appl
3	7	100.0	89	3 US-08-793-408-18	Sequence 18, Appl
4	7	100.0	89	3 US-09-139-762A-18	Sequence 18, Appl

#### ALIGNMENTS

RESULT 1  
US-09-731-558-20  
; Sequence 20, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731.558  
; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:SBS9  
; OTHER INFORMATION: recognition helix  
US-09-731-558-20

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRSNLTR 7  
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Db 1 DRSNLTR 7

RESULT 2  
US-09-424-487B-11  
; Sequence 11, Application US/09424487B  
; Patent No. 6746839  
; GENERAL INFORMATION:  
; APPLICANT: CHOO, YEN  
; APPLICANT: KLUG, AARON  
; APPLICANT: ISALAN, MARK  
; TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS  
; FILE REFERENCE: 71278/264975  
; CURRENT APPLICATION NUMBER: US/09/424,487B  
; CURRENT FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: GB 9710809.6  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: PCT/GB98/01512  
; PRIOR FILING DATE: 1998-05-26  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger  
; OTHER INFORMATION: peptide  
US-09-424-487B-11

Query Match 100.0%; Score 7; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.064;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRSNLTR 7  
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Db 12 DRSNLTR 18

RESULT 3  
US-08-793-408-18  
; Sequence 18, Application US/08793408  
; Patent No. 6007988  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Sanchez Garcia, Isidro  
; TITLE OF INVENTION: Improvements in or Relating to  
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,408
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-793-408-18

Query Match 100.0%; Score 7; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 74 DRSNLTR 80

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Job time : 15.9 secs

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; COMPUTER: IBM PC compatible
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; SOFTWARE: Word Perfect
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; APPLICATION NUMBER: US/08/793,408
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-793-408-18

Query Match 100.0%; Score 7; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRSNLTR 7
Db 74 DRSNLTR 80

RESULT 4
US-09-139-762A-18
; Sequence 18, Application US/09139762A
; Patent No. 6013453
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Sanchez Garcia, Isidro
; TITLE OF INVENTION: Improvements in or Relating to
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
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OM protein - protein search, using sw model

Run on: December 27, 2004, 18:12:11 ; Search time 15.9 Seconds  
(without alignments)  
29.197 Million cell updates/sec

Title: US-09-846-033B-55  
Perfect score: 7  
Sequence: 1 DRSNLTR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
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6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4 US-09-731-558-20	Sequence 20, Appl
2	7	100.0	27	4 US-09-424-487B-11	Sequence 11, Appl
3	7	100.0	89	3 US-08-793-408-18	Sequence 18, Appl
4	7	100.0	89	3 US-09-139-762A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1  
US-09-731-558-20  
; Sequence 20, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558  
; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:SBS9  
; OTHER INFORMATION: recognition helix  
US-09-731-558-20

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTR 7  
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Db 1 DRSNLTR 7

RESULT 2  
US-09-424-487B-11  
; Sequence 11, Application US/09424487B  
; Patent No. 6746838  
; GENERAL INFORMATION:  
; APPLICANT: CHOO, YEN  
; APPLICANT: KLUG, AARON  
; APPLICANT: ISALAN, MARK  
; TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS  
; FILE REFERENCE: 71278/264975  
; CURRENT APPLICATION NUMBER: US/09/424,487B  
; CURRENT FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: GB 9710809.6  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: PCT/GB98/01512  
; PRIOR FILING DATE: 1998-05-26  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger  
; OTHER INFORMATION: peptide  
US-09-424-487B-11

Query Match 100.0%; Score 7; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.064;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTR 7  
|||||||  
Db 12 DRSNLTR 18

RESULT 3  
US-08-793-408-18  
; Sequence 18, Application US/08793408  
; Patent No. 6007988  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Sanchez Garcia, Isidro  
; TITLE OF INVENTION: Improvements in or Relating to  
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:

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; FILING DATE:
; CLASSIFICATION: 435
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; FILING DATE: 17-AUG-1995
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; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-793-408-18

Query Match 100.0%; Score 7; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRSNLTR 7
Db 74 DRSNLTR 80

Search completed: December 27, 2004, 19:21:22
Job time : 16.9 secs
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,408
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-793-408-18

Query Match 100.0%; Score 7; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRSNLTR 7
Db 74 DRSNLTR 80

RESULT 4
US-09-139-762A-18
; Sequence 18, Application US/09139762A
; Patent No. 6013453
; GENERAL INFORMATION:
; APPLICANT: Chcoo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Sanchez Garcia, Isidro
; TITLE OF INVENTION: Improvements in or Relating to
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 18:12:11 ; Search time 15.9 Seconds  
(without alignments)  
29.197 Million cell updates/sec

Title: US-09-846-033B-54  
Perfect score: 7  
Sequence: 1 DRSHLTR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	7	100.0	89	3	US-08-793-408-18
3	7	100.0	89	3	US-09-139-762A-18

ALIGNMENTS

RESULT 1  
US-09-424-487B-10  
; Sequence 10, Application US/09424487B  
; Patent No. 674683B  
; GENERAL INFORMATION:  
; APPLICANT: CHOO, YEN  
; APPLICANT: KLUG, AARON  
; APPLICANT: ISALAN, MARK  
; TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS  
; FILE REFERENCE: 71278/264975  
; CURRENT APPLICATION NUMBER: US/09/424,487B  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: GB 9710809.6  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: PCT/GB98/01512  
; PRIOR FILING DATE: 1998-05-26  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10

; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger  
; OTHER INFORMATION: Peptide  
; US-09-424-487B-10

Query Match 100.0%; Score 7; DB 4; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSHLTR 7  
Db 12 DRSHLTR 18

RESULT 2

US-08-793-408-18  
; Sequence 18, Application US/08793408  
; Patent No. 6007988  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Sanchez Garcia, Isidro  
; TITLE OF INVENTION: Improvements in or Relating to  
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,408  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: PCT/GB95/01949  
; APPLICATION NUMBER: PCT/GB95/01949  
; FILING DATE: 17-AUG-1995  
; PRIOR APPLICATION DATA: GB 9514698.1  
; APPLICATION NUMBER: GB 9514698.1  
; FILING DATE: 18-JUL-1995  
; PRIOR APPLICATION DATA: GB 9422534.9  
; APPLICATION NUMBER: GB 9422534.9  
; FILING DATE: 08-NOV-1994  
; PRIOR APPLICATION DATA: GB 9416880.4  
; APPLICATION NUMBER: GB 9416880.4  
; FILING DATE: 20-AUG-1994  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 89 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein

US-08-793-408-18  
Query Match 100.0%; Score 7; DB 3; Length 89;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSHLTR 7  
Db 46 DRSHLTR 52

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RESULT 3
US-09-139-762A-18
; Sequence 18, Application US/09139762A
; Patent No. 6013453
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Sanchez Garcia, Isidro
; TITLE OF INVENTION: Improvements in or Relating to
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-139-762A-18
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Query Match      100.0%; Score 7; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DRSHLTR 7
Db      46 DRSHLTR 52
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Search completed: December 27, 2004, 19:21:21
Job time : 15.9 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 18:12:11 ; Search time 15.9 seconds  
(without alignments)  
29.197 Million cell updates/sec

Title: US-09-846-033B-51  
Perfect score: 7  
Sequence: 1 RSDHLTT 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 59

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
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5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	7	100.0	10	3	US-09-139-762A-53
4	7	100.0	20	1	US-08-040-548-19
5	7	100.0	20	1	US-08-466-344-19
6	7	100.0	21	4	US-09-229-007A-95
7	7	100.0	21	4	US-10-113-424-95
8	7	100.0	26	2	US-08-620-151-111
9	7	100.0	28	1	US-08-040-548-34
10	7	100.0	28	1	US-08-466-344-34
11	7	100.0	28	3	US-09-058-459-1
12	7	100.0	28	3	US-09-127-926-1
13	7	100.0	28	3	US-09-037-179B-15
14	7	100.0	28	4	US-09-240-179-2
15	7	100.0	28	4	US-09-714-357-1
16	7	100.0	28	4	US-09-500-700-70
17	7	100.0	28	4	US-09-716-637-13
18	7	100.0	59	1	US-08-040-548-7
19	7	100.0	59	1	US-08-466-344-7
20	7	100.0	85	4	US-09-229-007A-8
21	7	100.0	85	4	US-10-113-424-8
22	7	100.0	85	6	5206152-3
23	7	100.0	87	4	US-10-057-552-1
24	7	100.0	89	1	US-08-040-548-8
25	7	100.0	89	1	US-08-466-344-8
26	7	100.0	91	3	US-08-863-813A-5
27	7	100.0	91	3	US-08-676-318A-5

28	7	100.0	91	4	US-09-500-700-5	Sequence 5, Appli
29	7	100.0	109	2	US-08-224-482-11	Sequence 11, Appl
30	7	100.0	153	3	US-08-863-813A-34	Sequence 34, Appl
31	7	100.0	153	3	US-08-863-813A-36	Sequence 36, Appl
32	7	100.0	153	3	US-08-676-318A-34	Sequence 34, Appl
33	7	100.0	153	3	US-08-676-318A-36	Sequence 36, Appl
34	7	100.0	153	4	US-09-500-700-34	Sequence 34, Appl
35	7	100.0	153	4	US-09-500-700-36	Sequence 36, Appl
36	7	100.0	181	3	US-08-863-813A-44	Sequence 44, Appl
37	7	100.0	181	3	US-08-676-318A-44	Sequence 44, Appl
38	7	100.0	181	4	US-09-500-700-44	Sequence 44, Appl
39	7	100.0	387	2	US-08-224-482-8	Sequence 8, Appli
40	7	100.0	387	4	US-09-538-092-1278	Sequence 1278, Ap
41	7	100.0	453	6	5206152-7	Patent No. 5206152
42	7	100.0	455	2	US-08-224-482-6	Sequence 6, Appli
43	7	100.0	456	1	US-08-040-548-2	Sequence 2, Appli
44	7	100.0	456	1	US-08-466-344-2	Sequence 2, Appli
45	7	100.0	456	4	US-09-919-039-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1  
US-09-614-679A-19  
; Sequence 19, Application US/09614679A  
; Patent No. 6492117  
; GENERAL INFORMATION:  
; APPLICANT: CHOO, YEN  
; APPLICANT: ISALAN, MARK  
; APPLICANT: PATEL, SACHIN  
; APPLICANT: BALASUBRAMANIAN, SHANKAR  
; APPLICANT: LIU, XIAOHAI  
; TITLE OF INVENTION: MOLECULES  
; FILE REFERENCE: 71278/271599  
; CURRENT APPLICATION NUMBER: US/09/614,679A  
; CURRENT FILING DATE: 2000-07-12  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
; OTHER INFORMATION: peptide  
US-09-614-679A-19

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 1 RSDHLTT 7

RESULT 2  
US-09-139-762A-19  
; Sequence 19, Application US/09139762A  
; Patent No. 6013453  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Sanchez Garcia, Isidro  
; TITLE OF INVENTION: Improvements in or Relating to  
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
; NUMBER OF SEQUENCES: 125  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.

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; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-139-762A-19

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7
Db 1 RSDHLTT 7

RESULT 3
US-09-139-762A-53
; Sequence 53, Application US/09139762A
; Patent No. 6013453
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Sanchez Garcia, Isidro
; TITLE OF INVENTION: Improvements in or Relating to
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Suto, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7
Db 1 RSDHLTT 7

RESULT 4
US-08-040-548-19
; Sequence 19, Application US/08040548
; Patent No. 5763209
; GENERAL INFORMATION:
; APPLICANT: Sukhatme, Vikas P.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
; TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5763209th Clark Street, Suite 800
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/040,548
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coughlin, Daniel F.
; REGISTRATION NUMBER: 36,111
; REFERENCE/DOCKET NUMBER: aircd067
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 744-0090
; TELEFAX: (312) 245-4961
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-040-548-19

Query Match 100.0%; Score 7; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]

ADDRESSEE: BRINKS, HOFER, GILSON & LIONE  
STREET: NBC Tower - Suite 3600, 455 N. Cityfront  
STREET: Plaza Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60611-5599  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,151  
FILING DATE: 22-MAR-1996  
CLASSIFICATION: 422  
ATTORNEY/AGENT INFORMATION:  
NAME: Shannon, Karen L.  
REGISTRATION NUMBER: 36,675  
REFERENCE/DOCKET NUMBER: 8597/6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-321-4200  
TELEFAX: 312-321-4299  
INFORMATION FOR SEQ ID NO: 111:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-620-151-111

Query Match 100.0%; Score 7; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7  
Dbb 13 RSDHLTT 19

RESULT 9  
US-08-040-548-34  
Sequence 34, Application US/08040548  
Patent No. 5763209  
GENERAL INFORMATION:  
APPLICANT: Sukhatme, Vikas P.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE  
FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5763209th Clark Street, Suite 800  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/040,548  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coughlin, Daniel F.  
REGISTRATION NUMBER: 36,111  
REFERENCE/DOCKET NUMBER: arcd067  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 744-0090  
TELEFAX: (312) 245-4961

INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-040-548-34

Query Match 100.0%; Score 7; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7  
Dbb 9 RSDHLTT 15

RESULT 10  
US-08-466-344-34  
Sequence 34, Application US/08466344  
Patent No. 5773583  
GENERAL INFORMATION:  
APPLICANT: Sukhatme, Vikas P.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE  
FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5773583th Clark Street, Suite 800  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,344  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/040,548  
FILING DATE: 31-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coughlin, Daniel F.  
REGISTRATION NUMBER: 36,111  
REFERENCE/DOCKET NUMBER: arcd067  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 744-0090  
TELEFAX: (312) 245-4961  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-466-344-34

Query Match 100.0%; Score 7; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7  
Dbb 9 RSDHLTT 15

RESULT 11  
US-09-058-459-1

```

; Sequence 1, Application US/09058459
; Patent No. 6188965
; GENERAL INFORMATION:
; APPLICANT: Mayo, Stephen L.
; APPLICANT: Bahiyat, Bassil I.
; APPLICANT: Gordon, D. B.
; APPLICANT: Street, Arthur
; TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN
; FILE REFERENCE: A65353-3/RT/RMS/SJR
; CURRENT APPLICATION NUMBER: US/09/058,459
; CURRENT FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: 60/043,464
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/054,678
; PRIOR FILING DATE: 1997-08-04
; PRIOR APPLICATION NUMBER: 60/061,097
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Mouse
; US-09-058-459-1

Query Match 100.0%; Score 7; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
Db 14 RSDHLTT 20

RESULT 12
US-09-127-926-1
; Sequence 1, Application US/09127926
; Patent No. 6269312
; GENERAL INFORMATION:
; APPLICANT: Mayo, Stephen L.
; APPLICANT: Bahiyat, Bassil I.
; APPLICANT: Gordon, D. Benjamin
; APPLICANT: Street, Arthur
; APPLICANT: Su, Yaoying
; TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
; FILE REFERENCE: A65353-4/RT/RMS/SJR
; CURRENT APPLICATION NUMBER: US/09/127,926
; CURRENT FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/043,464
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/054,678
; PRIOR FILING DATE: 1997-08-04
; PRIOR APPLICATION NUMBER: 60/061,097
; PRIOR FILING DATE: 1997-10-03
; PRIOR APPLICATION NUMBER: 09/058,459
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/087,561
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Mouse
; US-09-127-926-1

Query Match 100.0%; Score 7; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
Db 14 RSDHLTT 20
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RESULT 13
US-09-037-179B-15
; Sequence 15, Application US/09037179B
; Patent No. 6316599
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; FILE REFERENCE: 0050.1312-011
; CURRENT APPLICATION NUMBER: US/09/037,179B
; CURRENT FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 08/102,942
; PRIOR FILING DATE: 1993-08-02
; PRIOR APPLICATION NUMBER: US 07/614,161
; PRIOR FILING DATE: 1990-11-13
; PRIOR APPLICATION NUMBER: US 07/435,780
; PRIOR FILING DATE: 1989-11-13
; PRIOR APPLICATION NUMBER: US 07/795,323
; PRIOR FILING DATE: 1994-09-27
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-037-179B-15

Query Match 100.0%; Score 7; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
Db 17 RSDHLTT 23

RESULT 14
US-09-240-179-2
; Sequence 2, Application US/09240179
; Patent No. 6410248
; GENERAL INFORMATION:
; APPLICANT: Greisman, Harvey A.
; APPLICANT: Pabo, Carl O.
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: A General Strategy for Selecting High-Affinity Zinc
; TITLE OF INVENTION: Finger Proteins for Diverse DNA Target Sites
; FILE REFERENCE: 019496-000220US
; CURRENT APPLICATION NUMBER: US/09/240,179
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: US 60/073,223
; EARLIER FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Zif268 zinc
; finger 2
; US-09-240-179-2
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Query Match 100.0%; Score 7; DB 4; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7  
|||  
Db 13 RSDHLTT 19

RESULT 15  
US-09-714-357-1  
; Sequence 1, Application US/09714357  
; Patent No. 6708120  
; GENERAL INFORMATION:  
; APPLICANT: Mayo, Stephen L.  
; APPLICANT: Dahiyat, Bassil I.  
; APPLICANT: Gordon, D. B.  
; APPLICANT: Street, Arthur  
; TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN  
; FILE REFERENCE: A65353-3/RFT/RMS/SJR  
; CURRENT APPLICATION NUMBER: US/09/714,357  
; CURRENT FILING DATE: 2000-11-15  
; PRIOR APPLICATION NUMBER: 09/058,459  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: 60/054,678  
; PRIOR FILING DATE: 1997-08-04  
; PRIOR APPLICATION NUMBER: 60/061,097  
; PRIOR FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-714-357-1

Query Match 100.0%; Score 7; DB 4; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7  
|||  
Db 14 RSDHLTT 20

Search completed: December 27, 2004, 19:21:21  
Job time : 16.9 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 18:12:11 ; Search time 15.9 Seconds  
(without alignments)  
29.197 Million cell updates/sec

Title: US-09-846-033B-50  
Perfect score: 7  
Sequence: 1 RSDALTR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-12
					Sequence 12, Appl

ALIGNMENTS

RESULT 1  
US-09-731-558-12  
; Sequence 12, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558  
; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 7  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SBS1  
; OTHER INFORMATION: recognition helix  
US-09-731-558-12

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDALTR 7  
|||  
Db 1 RSDALTR 7

Search completed: December 27, 2004, 19:21:20  
Job time : 15.9 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:31 ; Search time 15.8 Seconds  
(without alignments)  
29.381 Million cell updates/sec

Title: US-09-846-033B-46  
Perfect score: 7  
Sequence: 1 QSSNLAR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfilees1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-19
2	7	100.0	7	4	US-09-716-637-32

#### ALIGNMENTS

RESULT 1  
US-09-731-558-19  
; Sequence 19, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558  
; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 7

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:SBS8  
; OTHER INFORMATION: recognition helix  
US-09-731-558-19

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSSNLAR 7  
| | | | |  
Db 1 QSSNLAR 7

RESULT 2  
US-09-716-637-32  
; Sequence 32, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-IV F1  
US-09-716-637-32

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSSNLAR 7  
| | | | |  
Db 1 QSSNLAR 7

Search completed: December 27, 2004, 18:12:06  
Job time : 15.8 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:30 ; Search time 66.75 Seconds  
(without alignments)  
37.620 Million cell updates/sec

Title: US-09-846-033B-45  
Perfect score: 7  
Sequence: 1 TTSLNRR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 7

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Genesecp1980s:\*
- 2: Genesecp1990s:\*
- 3: Genesecp2000s:\*
- 4: Genesecp2001s:\*
- 5: Genesecp2002s:\*
- 6: Genesecp2003as:\*
- 7: Genesecp2003bs:\*
- 8: Genesecp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	5 ABP49026	Abp49026 Zinc fing
2	7	100.0	7	5 ABP48774	Abp48774 Zinc fing
3	7	100.0	7	5 ABP48777	Abp48777 Zinc fing
4	7	100.0	7	5 ABP48780	Abp48780 Zinc fing
5	7	100.0	7	5 ABP49029	Abp49029 Zinc fing
6	7	100.0	7	5 ABP48396	Abp48396 Zinc fing
7	7	100.0	7	5 ABP49134	Abp49134 Zinc fing
8	7	100.0	7	5 ABP48397	Abp48397 Zinc fing
9	7	100.0	7	5 ABP49056	Abp49056 Zinc fing
10	7	100.0	7	5 ABP48398	Abp48398 Zinc fing
11	7	100.0	7	5 ABB07125	Abb07125 Human veg
12	7	100.0	7	5 AAB47808	Aab47808 VEGF3a/1
13	7	100.0	7	5 AAB47802	Aab47802 VEGF-1 z1
14	7	100.0	7	5 ABJ03904	Abj03904 Human VEG
15	7	100.0	7	5 ABJ03800	Abj03800 Human VEG
16	7	100.0	7	5 ABJ03802	Abj03802 Human VEG
17	7	100.0	7	5 ABJ03801	Abj03801 Human VEG
18	7	100.0	7	6 AAE30448	Aae30448 VEGF spec
19	7	100.0	7	6 ABO01200	Ab01200 Human VEG
20	7	100.0	7	6 ABO01097	Ab01097 Human VEG
21	7	100.0	7	6 ABO01096	Ab01096 Human VEG
22	7	100.0	7	6 ABO01098	Ab01098 Human VEG
23	7	100.0	7	6 ABO14460	Ab014460 Human VEG
24	7	100.0	7	6 ABO14461	Ab014461 Human VEG
25	7	100.0	7	6 ABO14462	Ab014462 Human VEG

26	7	100.0	7	6 ABO14564	Ab014564 Human VEG
27	7	100.0	7	7 ADA62761	Ada62761 Zinc fing
28	7	100.0	7	7 ADA62760	Ada62760 Zinc fing
29	7	100.0	7	7 ADA62844	Ada62844 Zinc fing
30	7	100.0	7	7 ADA62879	Ada62879 Zinc fing
31	7	100.0	7	7 ADA62222	Ada62222 Zinc fing
32	7	100.0	7	7 ADA62759	Ada62759 Zinc fing
33	7	100.0	7	7 ADA62224	Ada62224 Zinc fing
34	7	100.0	7	7 ADA62223	Ada62223 Zinc fing
35	7	100.0	7	7 ADA62843	Ada62843 Zinc fing
36	7	100.0	7	7 ADA62853	Ada62853 Zinc fing
37	7	100.0	7	7 ADM21047	Adm21047 Synthetic
38	7	100.0	7	7 ADM21057	Adm21057 Synthetic
39	7	100.0	7	7 ADM20965	Adm20965 Synthetic
40	7	100.0	7	7 ADM21048	Adm21048 Synthetic
41	7	100.0	7	7 ADM20426	Adm20426 Synthetic
42	7	100.0	7	7 ADM20964	Adm20964 Synthetic
43	7	100.0	7	7 ADM20428	Adm20428 Synthetic
44	7	100.0	7	7 ADM20427	Adm20427 Synthetic
45	7	100.0	7	7 ADM21083	Adm21083 Synthetic

ALIGNMENTS

RESULT 1  
ABP49026  
ID ABP49026 standard; peptide; 7 AA.  
AC ABP49026;  
XX  
DT 28-AUG-2002 (first entry)  
DE Zinc finger protein related peptide motif SEQ ID NO:814.  
XX  
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200242459-A2.  
XX  
PD 30-MAY-2002.  
XX  
PF 20-NOV-2001; 2001WO-US043438.  
XX  
PR 20-NOV-2000; 2000US-00716637.  
XX  
(SANG-) SANGAMO BIOSCIENCES INC.  
Liu Q;  
WPI; 2002-500284/53.  
New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.  
Example 1; Page 45; 81pp; English.

The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target sub-site. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target sub-site, selecting the F2 zinc finger such that it binds to the S2 target sub-site, and selecting the F3 zinc finger such that it binds to the S3 target sub-site, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target sub-sites having the nucleotide G in the 5'-most position of the sub-site. (I) is useful in studying gene function, and for human therapeutics and plant

CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
 CC modulate the expression of a target region within a subject, in  
 CC diagnostic methods for sequence specific detection of target nucleic acid  
 CC in a sample, and in assays to determined the phenotype and function of  
 CC gene expression. (I) has improved affinity and specificity for their  
 CC target sequences, as well as enhanced biological activity. ABQ71213 to  
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
 CC finger peptides which are given in the exemplification of the present  
 CC invention  
 XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTSLRR 7  
 |||||  
 Db 1 TTSLRR 7

RESULT 2  
 ABP48774  
 ID ABP48774 standard; peptide; 7 AA.

XX AC ABP48774;  
 XX DT 28-AUG-2002 (first entry)  
 XX DE Zinc finger protein related peptide motif SEQ ID NO:730.  
 XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN WO200242459-A2.  
 XX PD 30-MAY-2002.

XX PF 20-NOV-2001; 2001WO-US043438.  
 XX PR 20-NOV-2000; 2000US-00716637.  
 XX PA (SANG-) SANGAMO BIOSCIENCES INC.

XX PI Liu Q;  
 XX DR WPI; 2002-500284/53.

XX PT New zinc finger protein that binds to target site, useful in studying  
 PT gene function and for human therapeutics and plant engineering, comprises  
 PT first, second and third zinc fingers, ordered from N- to C-terminus.  
 XX Example 1; Page 42; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a  
 CC target site, comprising a first (F1), a second (F2), and a third (F3)  
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide  
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it  
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such  
 CC that it binds to the S3 target subsite, thus designing (I) that binds to  
 CC a target site. (I) is useful for recognition of triplet target subsites  
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is  
 CC useful in studying gene function, and for human therapeutics and plant  
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
 CC modulate the expression of a target region within a subject, in  
 CC diagnostic methods for sequence specific detection of target nucleic acid  
 CC in a sample, and in assays to determined the phenotype and function of

CC gene expression. (I) has improved affinity and specificity for their  
 CC target sequences, as well as enhanced biological activity. ABQ71213 to  
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
 CC finger peptides which are given in the exemplification of the present  
 CC invention  
 XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTSLRR 7  
 |||||  
 Db 1 TTSLRR 7

RESULT 3  
 ABP48777

ID ABP48777 standard; peptide; 7 AA.

XX AC ABP48777;  
 XX DT 28-AUG-2002 (first entry)  
 XX DE Zinc finger protein related peptide motif SEQ ID NO:731.  
 XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN WO200242459-A2.  
 XX PD 30-MAY-2002.

XX PF 20-NOV-2001; 2001WO-US043438.  
 XX PR 20-NOV-2000; 2000US-00716637.

XX PA (SANG-) SANGAMO BIOSCIENCES INC.

XX PI Liu Q;

XX DR WPI; 2002-500284/53.

XX PT New zinc finger protein that binds to target site, useful in studying  
 PT gene function and for human therapeutics and plant engineering, comprises  
 PT first, second and third zinc fingers, ordered from N- to C-terminus.

XX Example 1; Page 42; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a  
 CC target site, comprising a first (F1), a second (F2), and a third (F3)  
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide  
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it  
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such  
 CC that it binds to the S3 target subsite, thus designing (I) that binds to  
 CC a target site. (I) is useful for recognition of triplet target subsites  
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is  
 CC useful in studying gene function, and for human therapeutics and plant  
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
 CC modulate the expression of a target region within a subject, in  
 CC diagnostic methods for sequence specific detection of target nucleic acid  
 CC in a sample, and in assays to determined the phenotype and function of  
 CC gene expression. (I), (II) or (III) is useful in therapeutic methods to  
 CC modulate the expression of a target region within a subject, in  
 CC diagnostic methods for sequence specific detection of target nucleic acid  
 CC in a sample, and in assays to determined the phenotype and function of

CC invention  
 XX Sequence 7 AA;  
 SQ

Query Match 100.0%; Score 7; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTSNLR 7  
 |||||  
 Db 1 TTSNLR 7

RESULT 4  
 ABP48780  
 ID ABP48780 standard; peptide; 7 AA.  
 AC  
 XX ABP48780;  
 XX  
 DT 28-AUG-2002 (first entry)  
 XX  
 DE Zinc finger protein related peptide motif SEQ ID NO:732.  
 XX  
 KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200242459-A2.  
 XX  
 PD 30-MAY-2002.  
 XX  
 PF 20-NOV-2001; 2001WO-US043438.  
 XX  
 PR 20-NOV-2000; 2000US-00716637.  
 XX  
 PA (SANG-) SANGAMO BIOSCIENCES INC.  
 XX  
 PI Liu Q;  
 XX  
 DR WPI; 2002-500284/53.  
 XX

New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.

Example 1; Page 42; 81pp; English.

CC The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention

Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 7; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTSNLR 7  
 |||||  
 Db 1 TTSNLR 7

RESULT 5  
 ABP49029  
 ID ABP49029 standard; peptide; 7 AA.  
 AC  
 XX ABP49029;  
 XX  
 DT 28-AUG-2002 (first entry)  
 XX  
 DE Zinc finger protein related peptide motif SEQ ID NO:815.  
 XX  
 KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200242459-A2.  
 XX  
 PD 30-MAY-2002.  
 XX  
 PF 20-NOV-2001; 2001WO-US043438.  
 XX  
 PR 20-NOV-2000; 2000US-00716637.  
 XX  
 PA (SANG-) SANGAMO BIOSCIENCES INC.  
 XX  
 PI Liu Q;  
 XX  
 DR WPI; 2002-500284/53.  
 XX

New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.

Example 1; Page 45; 81pp; English.

CC The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention

Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTSLRR 7  
 DB 1 TTSLRR 7

## RESULT 6

ABP48396  
 ID ABP48396 standard; peptide; 7 AA.

XX AC ABP48396;  
 XX DT 28-AUG-2002 (first entry)  
 XX DE Zinc finger protein related peptide motif SEQ ID NO:193.  
 XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN WO200242459-A2.  
 XX PD 30-MAY-2002.  
 XX PF 20-NOV-2001; 2001WO-US043438.  
 XX PR 20-NOV-2000; 2000US-00716637.  
 XX PA (SANG-) SANGAMO BIOSCIENCES INC.  
 XX PI Liu Q;  
 XX DR WPI; 2002-500284/53.

XX PT New zinc finger protein that binds to target site, useful in studying  
 PT gene function and for human therapeutics and plant engineering, comprises  
 PT first, second and third zinc fingers, ordered from N- to C-terminus.  
 XX PS Example 1; Page 38; 8lpp; English.  
 CC The present invention describes a zinc finger protein (I) that binds to a  
 CC target site, comprising a first (F1), a second (F2), and a third (F3)  
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
 CC and a third (S3) target subsite. Also described are: (i) a polypeptide  
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it  
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such  
 CC that it binds to the S3 target subsite, thus designing (I) that binds to  
 CC a target site. (I) is useful for recognition of triplet target subsites  
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is  
 CC useful in studying gene function, and for human therapeutics and plant  
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
 CC modulate the expression of a target region within a subject, in  
 CC diagnostic methods for sequence specific detection of target nucleic acid  
 CC in a sample, and in assays to determine the phenotype and function of  
 CC gene expression. (I) has improved affinity and specificity for their  
 CC target sequences, as well as enhanced biological activity. ABQ71213 to  
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
 CC finger peptides which are given in the exemplification of the present  
 CC invention

## Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0;

QY 1 TTSLRR 7  
 DB 1 TTSLRR 7

## RESULT 7

ABP49134  
 ID ABP49134 standard; peptide; 7 AA.

XX AC ABP49134;  
 XX DT 28-AUG-2002 (first entry)  
 XX DE Zinc finger protein related peptide motif SEQ ID NO:850.  
 XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN WO200242459-A2.  
 XX PD 30-MAY-2002.  
 XX PF 20-NOV-2001; 2001WO-US043438.  
 XX PR 20-NOV-2000; 2000US-00716637.  
 XX PA (SANG-) SANGAMO BIOSCIENCES INC.  
 XX PI Liu Q;  
 XX DR WPI; 2002-500284/53.

XX PT New zinc finger protein that binds to target site, useful in studying  
 PT gene function and for human therapeutics and plant engineering, comprises  
 PT first, second and third zinc fingers, ordered from N- to C-terminus.  
 XX PS Example 1; Page 46; 8lpp; English.  
 CC The present invention describes a zinc finger protein (I) that binds to a  
 CC target site, comprising a first (F1), a second (F2), and a third (F3)  
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
 CC and a third (S3) target subsite. Also described are: (i) a polypeptide  
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it  
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such  
 CC that it binds to the S3 target subsite, thus designing (I) that binds to  
 CC a target site. (I) is useful for recognition of triplet target subsites  
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is  
 CC useful in studying gene function, and for human therapeutics and plant  
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
 CC modulate the expression of a target region within a subject, in  
 CC diagnostic methods for sequence specific detection of target nucleic acid  
 CC in a sample, and in assays to determine the phenotype and function of  
 CC gene expression. (I) has improved affinity and specificity for their  
 CC target sequences, as well as enhanced biological activity. ABQ71213 to  
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
 CC finger peptides which are given in the exemplification of the present  
 CC invention

## Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0;

QY 1 TTSLRR 7  
 DB 1 TTSLRR 7

## RESULT 8

ABP48397  
 ID ABP48397 standard; peptide; 7 AA.

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XX ABP48397;
XX AC
XX 28-AUG-2002 (first entry)
XX DE
XX Zinc finger protein related peptide motif SEQ ID NO:194.
XX DT
XX Zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX KW
XX Homo sapiens.
XX OS Synthetic.
XX PN WO200242459-A2.
XX PD
XX 30-MAY-2002.
XX PF
XX 20-NOV-2001; 2001WO-US043438.
XX PR
XX 20-NOV-2000; 2000US-00716637.
XX PA (SANG-) SANGAMO BIOSCIENCES INC.
XX PI Liu Q;
XX WPI; 2002-500284/53.
XX New zinc finger protein that binds to target site, useful in studying
XX gene function and for human therapeutics and plant engineering, comprises
XX first, second and third zinc fingers, ordered from N- to C-terminus.
XX Example 1; Page 38; 81pp; English.
XX The present invention describes a zinc finger protein (I) that binds to a
XX target site, comprising a first (F1), a second (F2), and a third (F3)
XX zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
XX target site comprises, in 3'-5' direction, a first (S1), a second (S2),
XX and a third (S3) target subunit. Also described are: (1) a polypeptide
XX (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
XX (3) designing (M) (I) involves selecting the F1 zinc finger such that it
XX binds to the S1 target subunit, selecting the F2 zinc finger such that it
XX binds to the S2 target subunit, and selecting the F3 zinc finger such
XX that it binds to the S3 target subunit, thus designing (I) that binds to
XX a target site. (I) is useful for recognition of triplet target subunits
XX having the nucleotide G in the 5'-most position of the subunit. (I) is
XX useful in studying gene function, and for human therapeutics and plant
XX engineering. (I), (II) or (III) is useful in therapeutic methods to
XX modulate the expression of a target region within a subject, in
XX diagnostic methods for sequence specific detection of target nucleic acid
XX in a sample, and in assays to determine the phenotype and function of
XX gene expression. (I) has improved affinity and specificity for their
XX target sequences, as well as enhanced biological activity. AB071213 to
XX ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
XX finger peptides which are given in the exemplification of the present
XX invention
XX Sequence 7 AA;
XX
Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTSLNLR 7
DB 1 TTSLNLR 7

RESULT 9
ABP49056
ID ABP49056 standard; peptide; 7 AA.
XX AC ABP49056;
XX 28-AUG-2002 (first entry)
XX DT

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XX Zinc finger protein related peptide motif SEQ ID NO:824.
XX DE
XX Zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX KW
XX Homo sapiens.
XX OS Synthetic.
XX PN WO200242459-A2.
XX PD
XX 30-MAY-2002.
XX PF
XX 20-NOV-2001; 2001WO-US043438.
XX PR
XX 20-NOV-2000; 2000US-00716637.
XX PA (SANG-) SANGAMO BIOSCIENCES INC.
XX PI Liu Q;
XX WPI; 2002-500284/53.
XX New zinc finger protein that binds to target site, useful in studying
XX gene function and for human therapeutics and plant engineering, comprises
XX first, second and third zinc fingers, ordered from N- to C-terminus.
XX Example 1; Page 45; 81pp; English.
XX The present invention describes a zinc finger protein (I) that binds to a
XX target site, comprising a first (F1), a second (F2), and a third (F3)
XX zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
XX target site comprises, in 3'-5' direction, a first (S1), a second (S2),
XX and a third (S3) target subunit. Also described are: (1) a polypeptide
XX (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
XX (3) designing (M) (I) involves selecting the F1 zinc finger such that it
XX binds to the S1 target subunit, selecting the F2 zinc finger such that it
XX binds to the S2 target subunit, and selecting the F3 zinc finger such
XX that it binds to the S3 target subunit, thus designing (I) that binds to
XX a target site. (I) is useful for recognition of triplet target subunits
XX having the nucleotide G in the 5'-most position of the subunit. (I) is
XX useful in studying gene function, and for human therapeutics and plant
XX engineering. (I), (II) or (III) is useful in therapeutic methods to
XX modulate the expression of a target region within a subject, in
XX diagnostic methods for sequence specific detection of target nucleic acid
XX in a sample, and in assays to determine the phenotype and function of
XX gene expression. (I) has improved affinity and specificity for their
XX target sequences, as well as enhanced biological activity. AB071213 to
XX ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
XX finger peptides which are given in the exemplification of the present
XX invention
XX Sequence 7 AA;
XX
Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTSLNLR 7
DB 1 TTSLNLR 7

RESULT 10
ABP48398
ID ABP48398 standard; peptide; 7 AA.
XX AC ABP48398;
XX 28-AUG-2002 (first entry)
XX DT
XX Zinc finger protein related peptide motif SEQ ID NO:195.
XX DE
XX Zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX KW

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XX Homo sapiens.
OS Synthetic.
XX WO200242459-A2.
XX PD 30-MAY-2002.
XX PF 20-NOV-2001; 2001WO-US043438.
XX PR 20-NOV-2000; 2000US-00716637.
XX PA (SANG-) SANGAMO BIOSCIENCES INC.
XX PI Liu Q;
XX WI; 2002-500284/53.
XX DR New zinc finger protein that binds to target site, useful in studying
XX PT gene function and for human therapeutics and plant engineering, comprises
XX PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX PS Example 1; Page 38; 81pp; English.
XX CC The present invention describes a zinc finger protein (I) that binds to a
XX CC target site, comprising a first (F1), a second (F2), and a third (F3)
XX CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
XX CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
XX CC and a third (S3) target subsite. Also described are: (1) a polypeptide
XX CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
XX CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
XX CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
XX CC binds to the S2 target subsite, and selecting the F3 zinc finger such
XX CC that it binds to the S3 target subsite, thus designing (I) that binds to
XX CC a target site. (I) is useful for recognition of triplet target subsites
XX CC having the nucleotide G in the 5'-most position of the subsite. (I) is
XX CC useful in studying gene function, and for human therapeutics and plant
XX CC engineering. (I), (II) or (III) is useful in therapeutic methods to
XX CC modulate the expression of a target region within a subject, in
XX CC diagnostic methods for sequence specific detection of target nucleic acid
XX CC in a sample, and in assays to determine the phenotype and function of
XX CC gene expression. (I) has improved affinity and specificity for their
XX CC target sequences, as well as enhanced biological activity. ABQ71213 to
XX CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
XX CC finger peptides which are given in the exemplification of the present
XX CC invention
XX SQ Sequence 7 AA;
XX Query Match 100.0%; Score 7; DB 5; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 TTSLNRR 7
XX Db 1 TTSLNRR 7
XX RESULT 11
XX ABB07125
XX ID ABB07125 standard; peptide; 7 AA.
XX XX ABB07125;
XX AC ABB07125;
XX DT 13-MAR-2002 (first entry)
XX DE Human veg 1 protein zinc finger fragment F1.
XX KW VEGF; chromatin; cytostatic; vasotropic; antidiabetic; ophthalmological;
XX KW antirheumatic; antiarthritic; antipsoriatic; anti-HIV; anticlacking;
XX KW neuroprotective; nootropic; cerebroprotective; antibacterial; fungicide;
XX KW virucide; gene therapy; Veg 1; zinc finger.
XX XX

OS Homo sapiens.
XX PN WO200183793-A2.
XX XX PD 08-NOV-2001.
XX PF 27-APR-2001; 2001WO-US040616.
XX PR 28-APR-2000; 2000US-0200590P.
XX PR 28-AUG-2000; 2000US-0228523P.
XX XX (SANG-) SANGAMO BIOSCIENCES INC.
XX PA
XX PI Wolffe AP, Collingwood T;
XX XX WI; 2002-075165/10.
XX DR
XX PS Modification of chromatin structure for facilitating transcription,
XX PT replication and repair, comprises contacting chromatin with fusion
XX PT molecule comprising DNA binding domain and component of a chromatin
XX PT remodeling complex.
XX PS Example 1; Page 59; 99pp; English.
XX CC The invention provides a method of modifying a region of interest in
XX CC cellular chromatin that involves contacting the cellular chromatin with a
XX CC fusion molecule that binds to a binding site in the region of interest,
XX CC where the fusion molecule comprises a DNA binding domain and a component
XX CC of a chromatin remodeling complex or its functional fragment, which
XX CC modifies the region of interest. The method is useful for modifying a
XX CC region of interest, in particular a gene encoding a product such as
XX CC vascular endothelial growth factor, erythropoietin, androgen receptor,
XX CC peroxisome proliferator-activated receptor (PPAR-gamma2), p16, p53, pRb,
XX CC dystraphin and e-cadherin in cellular chromatin present in a plant,
XX CC animal or human cell. The chromatin modification facilitates detection of
XX CC sequence of interest comprising a single nucleotide polymorphism,
XX CC activation or repression of a gene of interest or recombination between
XX CC an exogenous nucleic acid and cellular chromatin. It also results in
XX CC generation of an accessible region in the cellular chromatin which
XX CC facilitates binding of an exogenous molecule such as polypeptides,
XX CC nucleic acids, small molecule therapeutics, minor groove binders, major
XX CC groove binders and intercalators. The fusion molecule may be used for
XX CC modulating expression of a gene and for binding an exogenous molecule to
XX CC a binding site located within a gene in cellular chromatin.
XX CC Polynucleotides encoding the fusion polypeptide are useful for gene
XX CC therapy to modulate gene expression, for therapeutic or prophylactic
XX CC applications, e.g., for treating cancer, ischemia, diabetic retinopathy,
XX CC macular degeneration, rheumatoid arthritis, psoriasis, HIV infection,
XX CC sickle cell anemia, Alzheimer's disease, muscular dystrophy, vascular
XX CC disease, neurodegenerative diseases, cystic fibrosis, stroke and for
XX CC inhibiting microorganisms, e.g., Chlamydia, Mycobacteria, Pneumococci,
XX CC infectious fungus, e.g., Candida sp. and viruses, e.g., hepatitis.
XX CC Sequences ABB07125-130 represent DNA-binding zinc fingers of the human
XX CC VEGF-A protein
XX SQ Sequence 7 AA;
XX Query Match 100.0%; Score 7; DB 5; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 TTSLNRR 7
XX Db 1 TTSLNRR 7
XX RESULT 12
XX AAB47808
XX ID AAB47808 standard; peptide; 7 AA.
XX XX AAB47808;
XX XX 25-MAR-2002 (first entry)
XX DT

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XX VEGF3a/1 zinc finger domain F4.  
 DE Target site; transcriptional effector protein; zinc finger domain; human;  
 XX vascular endothelial growth factor; VEGF; cellular chromatin;  
 KW gene expression; sequence-specific; DNA binding protein; phenotype;  
 KW copy number; p53; cancer; gene function.  
 XX Synthetic.  
 XX WO200183751-A2.  
 XX 08-NOV-2001.  
 XX 27-APR-2001; 2001WO-US013631.  
 XX 28-APR-2000; 2000US-0200590P.  
 XX (SANG-) SANGAMO BIOSCIENCES INC.  
 XX Raschke E, Wolffe AP, Case CC;  
 XX WPI; 2002-066534/09.  
 XX Binding an exogenous molecule (EM) to a binding site located within a  
 XX region of interest in chromatin, useful for modulating gene expression,  
 XX by identifying an EM target site within an accessible region and  
 XX introducing the EM into the cell.  
 XX Example 8; Page 25; 50pp; English.  
 XX The sequences given in AAB47802-16 represent zinc finger domains derived  
 XX from transcriptional effector proteins. These transcriptional effector  
 XX proteins were designed to bind to target sites derived from the  
 XX transcriptional initiation site of the human vascular endothelial growth  
 XX factor (VEGF) gene. Target site #1 was bound by a binding domain  
 XX containing six zinc fingers, named VEGF3a/1. Target site #2 was bound by  
 XX a three-finger zinc finger domain, VEGF-1, and a control six-finger  
 XX domain, GATA15.5, was designed to bind to target sequence #3. The zinc  
 XX finger containing proteins were used to demonstrate the method of the  
 XX invention for binding an exogenous molecule (EM) to a binding site (BS),  
 XX where the BS is located within a region of interest in cellular  
 XX chromatin. The method comprises identifying an accessible region within  
 XX the region of interest, identifying a target site for the EM within the  
 XX accessible region, and introducing the EM into the cell, where the EM  
 XX binds to the BS. The method is useful for modulating gene expression by  
 XX administering an exogenous molecule. The binding of an exogenous molecule  
 XX to a binding site in cellular chromatin can be used for detection of a  
 XX particular sequence. For example, an exogenous molecule, such as a  
 XX sequence-specific DNA binding protein, can be used to detect variant  
 XX alleles associated with a disease or with a particular phenotype in  
 XX patient samples and to detect the presence of pathological microorganisms  
 XX in clinical samples. Exogenous molecules can also be used to quantify  
 XX copy number of a gene in a sample. For example, detection of the loss of  
 XX one copy of a p53 gene in a clinical sample is an indicator of  
 XX susceptibility to cancer. The methods can also be used in assays to  
 XX determine gene function and to determine changes in phenotype resulting  
 XX from specific modulation of gene expression

Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTSLNLR 7  
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 Db 1 TTSLNLR 7

RESULT 13  
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 ID AAB47802 standard; peptide; 7 AA.

XX AAB47802;  
 AC 25-MAR-2002 (first entry)  
 DT VEGF-1 zinc finger domain F4.  
 DE Target site; transcriptional effector protein; zinc finger domain; human;  
 XX vascular endothelial growth factor; VEGF; cellular chromatin;  
 KW gene expression; sequence-specific; DNA binding protein; phenotype;  
 KW copy number; p53; cancer; gene function.  
 XX Synthetic.  
 XX WO200183751-A2.  
 XX 08-NOV-2001.  
 XX 27-APR-2001; 2001WO-US013631.  
 XX 28-APR-2000; 2000US-0200590P.  
 XX (SANG-) SANGAMO BIOSCIENCES INC.  
 XX Raschke E, Wolffe AP, Case CC;  
 XX WPI; 2002-066534/09.  
 XX Binding an exogenous molecule (EM) to a binding site located within a  
 XX region of interest in chromatin, useful for modulating gene expression,  
 XX by identifying an EM target site within an accessible region and  
 XX introducing the EM into the cell.  
 XX Example 8; Page 25; 50pp; English.  
 XX The sequences given in AAB47802-16 represent zinc finger domains derived  
 XX from transcriptional effector proteins. These transcriptional effector  
 XX proteins were designed to bind to target sites derived from the  
 XX transcriptional initiation site of the human vascular endothelial growth  
 XX factor (VEGF) gene. Target site #1 was bound by a binding domain  
 XX containing six zinc fingers, named VEGF3a/1. Target site #2 was bound by  
 XX a three-finger zinc finger domain, VEGF-1, and a control six-finger  
 XX domain, GATA15.5, was designed to bind to target sequence #3. The zinc  
 XX finger containing proteins were used to demonstrate the method of the  
 XX invention for binding an exogenous molecule (EM) to a binding site (BS),  
 XX where the BS is located within a region of interest in cellular  
 XX chromatin. The method comprises identifying an accessible region within  
 XX the region of interest, identifying a target site for the EM within the  
 XX accessible region, and introducing the EM into the cell, where the EM  
 XX binds to the BS. The method is useful for modulating gene expression by  
 XX administering an exogenous molecule. The binding of an exogenous molecule  
 XX to a binding site in cellular chromatin can be used for detection of a  
 XX particular sequence. For example, an exogenous molecule, such as a  
 XX sequence-specific DNA binding protein, can be used to detect variant  
 XX alleles associated with a disease or with a particular phenotype in  
 XX patient samples and to detect the presence of pathological microorganisms  
 XX in clinical samples. Exogenous molecules can also be used to quantify  
 XX copy number of a gene in a sample. For example, detection of the loss of  
 XX one copy of a p53 gene in a clinical sample is an indicator of  
 XX susceptibility to cancer. The methods can also be used in assays to  
 XX determine gene function and to determine changes in phenotype resulting  
 XX from specific modulation of gene expression

Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTSLNLR 7  
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 Db 1 TTSLNLR 7

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RESULT 14
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ID ABJ03904 standard; peptide; 7 AA.
XX
AC ABJ03904;
XX
DT 25-SEP-2002 (first entry)
XX
DE Human VEGF-targeted zinc finger protein fragment SEQ ID NO: 161.
XX
KW Zinc finger protein; angiogenesis; vasculogenesis; ischaemia;
KW diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth;
KW gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnerary;
KW antiulcer; cytostatic; antipsoriatic; antidiabetic; ophthalmological;
KW osteopathic; antiinfertility.
XX
OS Homo sapiens.
XX
PN WO200246412-A2.
XX
PD 13-JUN-2002.
XX
PF 06-DEC-2001; 2001WO-US046861.
XX
PR 07-DEC-2000; 2000US-00733604.
XX
PR 12-DEC-2000; 2000US-00736083.
XX
PR 30-APR-2001; 2001US-00846033.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Rebar E, Jamieson A, Liu Q, Liu P, Wolffe A, Eisenberg SP;
PI Jarvis E;
XX
DR WPI; 2002-527918/56.
XX
PT New zinc finger protein that binds to target site in vascular endothelial
PT growth factor gene, useful for modulating expression of the gene and for
PT treating atherosclerosis, ischemia, arthritis, wound or ulcer.
XX
PS Example 1; Page 104; 195pp; English.
XX
CC The present invention relates to a zinc finger protein that binds to a
CC target site in one or more vascular endothelial growth factor (VEGF)
CC genes. The protein is useful for modulating expression of a VEGF gene,
CC thereby regulating angiogenesis and vasculogenesis. This can be used to
CC treat atherosclerosis, ischaemia, arthritis, wounds, ulcers, tumours,
CC diabetic retinopathy or psoriasis. The present sequence is a peptide
CC shown in the invention
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTSLNRR 7
Db 1 TTSLNRR 7

RESULT 15
ABJ03800
ID ABJ03800 standard; peptide; 7 AA.
XX
AC ABJ03800;
XX
DT 25-SEP-2002 (first entry)
XX
DE Human VEGF-targeted zinc finger protein fragment SEQ ID NO: 43.
XX
KW Zinc finger protein; angiogenesis; vasculogenesis; ischaemia;
KW diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth;

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KW Gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnerary;
KW antiulcer; cytostatic; antipsoriatic; antidiabetic; ophthalmological;
XX osteopathic; antiinfertility.
XX Homo sapiens.
XX WO200246412-A2.
XX 13-JUN-2002.
XX 06-DEC-2001; 2001WO-US046861.
XX 07-DEC-2000; 2000US-00733604.
XX 12-DEC-2000; 2000US-00736083.
XX 30-APR-2001; 2001US-00846033.
XX (SANG-) SANGAMO BIOSCIENCES INC.
XX Rebar E, Jamieson A, Liu Q, Liu P, Wolffe A, Eisenberg SP;
XX Jarvis E;
XX WPI; 2002-527918/56.
XX New zinc finger protein that binds to target site in vascular endothelial
XX growth factor gene, useful for modulating expression of the gene and for
XX treating atherosclerosis, ischemia, arthritis, wound or ulcer.
XX Claim 4; Page 102; 195pp; English.
XX The present invention relates to a zinc finger protein that binds to a
XX target site in one or more vascular endothelial growth factor (VEGF)
XX genes. The protein is useful for modulating expression of a VEGF gene,
XX thereby regulating angiogenesis and vasculogenesis. This can be used to
XX treat atherosclerosis, ischaemia, arthritis, wounds, ulcers, tumours,
XX diabetic retinopathy or psoriasis. The present sequence is a peptide
XX shown in the invention
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTSLNRR 7
Db 1 TTSLNRR 7

Search completed: December 27, 2004, 18:06:48
Job time : 66.75 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:31 ; Search time 15.8 Seconds  
(without alignments)  
29.381 Million cell updates/sec

Title: US-09-846-033B-45  
Perfect score: 7  
Sequence: 1 TTSNLRR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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3:	/cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4:	/cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5:	/cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6:	/cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4 US-09-716-637-27	Sequence 27, Appl
2	7	100.0	99	4 US-09-229-037-15	Sequence 15, Appl
3	7	100.0	99	4 US-09-478-681-15	Sequence 15, Appl
4	7	100.0	99	4 US-09-779-233-3	Sequence 3, Appl
5	7	100.0	196	4 US-09-229-037-30	Sequence 30, Appl
6	7	100.0	196	4 US-09-478-681-30	Sequence 30, Appl
7	7	100.0	196	4 US-09-779-233-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1  
US-09-716-637-27  
; Sequence 27, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I Fl  
US-09-716-637-27

Query Match 100.0%; Score 7; DB 4; Length 7;  
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTSNLRR 7  
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Db 1 TTSNLRR 7

RESULT 2  
US-09-229-037-15  
; Sequence 15, Application US/09229037A  
; Patent No. 6534261  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George No. 6534261bert  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric Edward  
; APPLICANT: Spratt, Sharon Kaye  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using  
; FILE REFERENCE: 019496-002200US  
; CURRENT APPLICATION NUMBER: US/09/229,037A  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 99  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP  
; OTHER INFORMATION: construct targeting upstream 9-base pair target  
; OTHER INFORMATION: site in VEGF promoter  
US-09-229-037-15

Query Match 100.0%; Score 7; DB 4; Length 99;  
Best Local Similarity 100.0%; Pred. No. 0.91;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTSNLRR 7  
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Db 23 TTSNLRR 29

RESULT 3  
US-09-478-681-15  
; Sequence 15, Application US/09478681  
; Patent No. 6607882  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 43  
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; LENGTH: 99
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; FEATURE:
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; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-478-681-15

Query Match      100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTSNLR 7
Db 23 TTSNLR 29

RESULT 4
US-09-779-233-3
; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-779-233-3

Query Match      100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTSNLR 7
Db 23 TTSNLR 29

RESULT 5
US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-229-037-30

Query Match      100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTSNLR 7
Db 23 TTSNLR 29

RESULT 6
US-09-478-681-30
; Sequence 30, Application US/09478681
; Patent No. 6607882
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric E.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS
; FILE REFERENCE: 8325-0002.10 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/478,681
; CURRENT FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-478-681-30

Query Match      100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 120 TTSNLR 126

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; Sequence 18, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1
US-09-779-233-18

Query Match      100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTSNLR 7
Db 120 TTSNLR 126

RESULT 7
US-09-779-233-18
; Sequence 18, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1
US-09-779-233-18

Query Match      100.0%; Score 7; DB 4; Length 196;
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Qy 1 TTSNLR 7
Db 120 TTSNLR 126
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

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(without alignments)  
29.381 Million cell updates/sec

Title: US-09-846-033B-44  
Perfect score: 7  
Sequence: 1 TTSNLRR 7

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Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4 US-09-716-637-27	Sequence 27, Appl
2	7	100.0	99	4 US-09-229-037-15	Sequence 15, Appl
3	7	100.0	99	4 US-09-478-681-15	Sequence 15, Appl
4	7	100.0	99	4 US-09-779-233-3	Sequence 3, Appl
5	7	100.0	196	4 US-09-229-037-30	Sequence 30, Appl
6	7	100.0	196	4 US-09-478-681-30	Sequence 30, Appl
7	7	100.0	196	4 US-09-779-233-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1  
US-09-716-637-27  
; Sequence 27, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716.637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F1  
US-09-716-637-27

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Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
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RESULT 2

US-09-229-037-15  
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; Patent No. 6534261  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George No. 6534261bert  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric Edward  
; APPLICANT: Spratt, Sharon Kaye  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using  
; TITLE OF INVENTION: Zinc Finger Proteins  
; FILE REFERENCE: 019496-002200US  
; CURRENT APPLICATION NUMBER: US/09/229,037A  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
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; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP  
; OTHER INFORMATION: Construct targeting upstream 9-base pair target  
; OTHER INFORMATION: site in VEGF promoter  
US-09-229-037-15

Query Match 100.0%; Score 7; DB 4; Length 99;  
Best Local Similarity 100.0%; Pred. No. 0.91;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTSNLRR 7  
|||||  
Db 23 TTSNLRR 29

RESULT 3

US-09-478-681-15  
; Sequence 15, Application US/09478681  
; Patent No. 6607882  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15

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; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP
; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-478-681-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 23 TTSNLR 29

RESULT 4
US-09-779-233-3
; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTSNLR 7
DB 23 TTSNLR 29

RESULT 5
US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-229-037-30
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QY 1 TTSNLR 7
DB 120 TTSNLR 126

RESULT 6
US-09-478-681-30
; Sequence 30, Application US/09478681
; Patent No. 6607882
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric E.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; FILE REFERENCE: 8325-0002.10 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/478,681
; CURRENT FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-478-681-30
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Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTSNLR 7
DB 120 TTSNLR 126

RESULT 7
US-09-779-233-18
; Sequence 18, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1
US-09-779-233-18
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Query Match          100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTSNLR 7
DB 120 TTSNLR 126
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Search completed: December 27, 2004, 18:12:05  
Job time : 15.8 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:31 ; Search time 15.8 Seconds  
(without alignments)  
29.381 Million cell updates/sec

Title: US-09-846-033B-43  
Perfect score: 7  
Sequence: 1 TTSNLRR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	7	100.0	99	4 US-09-229-037-15	Sequence 15, Appl
3	7	100.0	99	4 US-09-478-681-15	Sequence 15, Appl
4	7	100.0	99	4 US-09-779-233-3	Sequence 3, Appl
5	7	100.0	196	4 US-09-229-037-30	Sequence 30, Appl
6	7	100.0	196	4 US-09-478-681-30	Sequence 30, Appl
7	7	100.0	196	4 US-09-779-233-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1  
US-09-716-637-27  
; Sequence 27, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F1  
US-09-716-637-27

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QY 1 TTSNLRR 7  
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Db 1 TTSNLRR 7

RESULT 2  
US-09-229-037-15  
; Sequence 15, Application US/09229037A  
; Patent No. 6534261  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George No. 6534261bert  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric Edward  
; APPLICANT: Spratt, Sharon Kaye  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using  
; TITLE OF INVENTION: Zinc Finger Proteins  
; FILE REFERENCE: 019496-002200US  
; CURRENT APPLICATION NUMBER: US/09/229,037A  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 99  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP  
; OTHER INFORMATION: construct targeting upstream 9-base pair target  
; OTHER INFORMATION: site in VEGF promoter  
US-09-229-037-15

Query Match 100.0%; Score 7; DB 4; Length 99;  
Best Local Similarity 100.0%; Pred. No. 0.91; 0; Indels 0; Gaps 0;  
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Db 23 TTSNLRR 29

RESULT 3  
US-09-478-681-15  
; Sequence 15, Application US/09478681  
; Patent No. 6607892  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
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; LENGTH: 99
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; ORGANISM: Artificial Sequence
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; FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP
;   OTHER INFORMATION: construct targeting upstream 9-base pair target
;   OTHER INFORMATION: site in VEGF promoter
US-09-478-681-15

Query Match      100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 23 TTSNLR 29

RESULT 4
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; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3

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Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTSNLR 7
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Db 23 TTSNLR 29

RESULT 5
US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpni to BamHI
US-09-229-037-30

Query Match      100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 120 TTSNLR 126

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; Sequence 30, Application US/09478681
; Patent No. 6607882
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric E.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS
; FILE REFERENCE: 8325-0002.10 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/478,681
; CURRENT FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpni to BamHI
US-09-478-681-30

Query Match      100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTSNLR 7
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Db 120 TTSNLR 126

RESULT 7
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; Sequence 18, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1
US-09-779-233-18

Query Match      100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTSNLR 7
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Db 120 TTSNLR 126
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Job time : 15.8 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:31 ; Search time 15.8 Seconds  
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Title: US-09-846-033B-42

Perfect score: 7

Sequence: 1 RSDNLTR 7

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	7	100.0	21	4	Sequence 97, Appl
4	7	100.0	88	4	US-10-113-424-97
5	7	100.0	88	4	Sequence 2, Appli
6	7	100.0	88	4	Sequence 2, Appli
7	7	100.0	97	4	Sequence 15, Appl
8	7	100.0	97	4	Sequence 15, Appl
9	7	100.0	97	4	Sequence 15, Appl
10	7	100.0	97	4	Sequence 15, Appl

#### ALIGNMENTS

RESULT 1  
US-09-229-007A-97  
; Sequence 97, Application US/09229007A  
; Patent No. 6453242  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Case, Casey C.  
; APPLICANT: Cox III, George N.  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger  
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins  
; TITLE OF INVENTION: to Bind to Preslected Sites  
; FILE REFERENCE: 019496-001800US

; CURRENT APPLICATION NUMBER: US/09/229,007A  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 97  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence  
; OTHER INFORMATION: (F1, F2, F3) from SBS design GL-8.3.1

US-09-229-007A-97

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Best Local Similarity 100.0%; Pred. No. 0.04;  
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QY 1 RSDNLTR 7

Db 15 RSDNLTR 21

#### RESULT 2

US-10-113-424-97

; Sequence 97, Application US/10113424

; Patent No. 6785613

; GENERAL INFORMATION:

; APPLICANT: Eisenberg, Stephen P.

; APPLICANT: Case, Casey C.

; APPLICANT: Cox III, George N.

; APPLICANT: Jamieson, Andrew

; APPLICANT: Rebar, Edward J.

; APPLICANT: Sangamo Biosciences, Inc.

; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger

; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins

; TITLE OF INVENTION: to Bind to Preslected Sites

; FILE REFERENCE: 019496-001800US

; CURRENT APPLICATION NUMBER: US/10/113,424

; CURRENT FILING DATE: 2002-03-28

; PRIOR APPLICATION NUMBER: US/09/229,007A

; PRIOR FILING DATE: 1999-01-12

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 97

; LENGTH: 21

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence

; OTHER INFORMATION: (F1, F2, F3) from SBS design GL-8.3.1

US-10-113-424-97

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Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDNLTR 7

Db 15 RSDNLTR 21

#### RESULT 3

US-09-851-271A-2

; Sequence 2, Application US/09851271A

; Patent No. 6733970

; GENERAL INFORMATION:

; APPLICANT: Gendag Limited

; APPLICANT: Rebar, Edward J.

; APPLICANT: Sangamo Biosciences, Inc.

; TITLE OF INVENTION: Screening System

; FILE REFERENCE: 674538-2003

; CURRENT APPLICATION NUMBER: US/09/851,271A

; CURRENT FILING DATE: 2001-05-08

; PRIOR APPLICATION NUMBER: PCT/GB99/03730

; FILE REFERENCE: 019496-001800US

; PRIOR APPLICATION NUMBER: GB9824544.2  
; PRIOR FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 88  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: ZN FING  
; LOCATION: (1)..(88)  
; OTHER INFORMATION: protein sequence encoding a zinc-finger domain  
US-09-851-271A-2

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US-09-424-487B-2  
; Sequence 2, Application US/09424487B  
; Patent No. 6746838  
; GENERAL INFORMATION:  
; APPLICANT: CHOO, YEN  
; APPLICANT: KLUG, AARON  
; APPLICANT: ISALAN, MARK  
; TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS  
; FILE REFERENCE: 71278/264975  
; CURRENT APPLICATION NUMBER: US/09/424,487B  
; CURRENT FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: GB 9710809.6  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: PCT/GB98/01512  
; PRIOR FILING DATE: 1998-05-26  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 88  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic amino acid  
US-09-424-487B-2

Query Match 100.0%; Score 7; DB 4; Length 88;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDNLTR 7  
Db 45 RSDNLTR 51

RESULT 5  
US-09-395-448-15  
; Sequence 15, Application US/09395448  
; Patent No. 6599692  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey C.  
; APPLICANT: Zhang, Lei  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Functional Genomics Using Zinc Finger Proteins  
; FILE REFERENCE: 019496-002000US  
; CURRENT APPLICATION NUMBER: US/09/395,448  
; CURRENT FILING DATE: 1999-03-14  
; PRIOR APPLICATION NUMBER: 09/229,007  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 09/229,037

; PRIOR FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 97  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: designed ZFP  
US-09-395-448-15

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Db 21 RSDNLTR 27

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US-09-925-796-15  
; Sequence 15, Application US/09925796  
; Patent No. 6777185  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey C.  
; APPLICANT: Zhang, Lei  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Functional Genomics Using Zinc Finger Proteins  
; FILE REFERENCE: 019496-002000US  
; CURRENT APPLICATION NUMBER: US/09/925,796  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/395,448  
; PRIOR FILING DATE: 1999-09-14  
; PRIOR APPLICATION NUMBER: 09/229,037  
; PRIOR FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
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; LENGTH: 97  
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; ORGANISM: Artificial Sequence  
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; OTHER INFORMATION: Description of Artificial Sequence: designed ZFP  
US-09-925-796-15

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Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7  
US-09-941-450-15  
; Sequence 15, Application US/09941450  
; Patent No. 6780590  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey C.  
; APPLICANT: Urnov, Fyodor  
; TITLE OF INVENTION: GENE IDENTIFICATION  
; FILE REFERENCE: S7.US3 / 8325-0007.20  
; CURRENT APPLICATION NUMBER: US/09/941,450  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 09/395,448  
; PRIOR FILING DATE: 1999-09-14  
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; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 97  
; TYPE: PRT



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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence:designed ZFP
US-09-941-450-15

Query Match      100.0%; Score 7; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      21 RSDNLTR 27
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Job time : 15.8 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:31 ; Search time 15.8 Seconds  
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29.381 Million cell updates/sec

Title: US-09-846-033B-41  
Sequence: 1 RSDHLAR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7  
Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	7	100.0	7	4 US-09-779-233-42	Sequence 42, Appl
2	7	100.0	100	4 US-09-248-796A-16192	Sequence 16192, A

ALIGNMENTS

RESULT 1  
US-09-779-233-42  
; Sequence 42, Application US/09779233  
; Patent No. 668958  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
; OTHER INFORMATION: helix  
US-09-779-233-42

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7  
| | | | |  
DB 1 RSDHLAR 7

RESULT 2

US-09-248-796A-16192  
; Sequence 16192, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 16192  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-16192

Query Match 100.0%; Score 7; DB 4; Length 100;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7  
| | | | |  
DB 57 RSDHLAR 63

Search completed: December 27, 2004, 18:12:05  
Job time : 16.8 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run On: December 27, 2004, 17:02:31 ; Search time 15.8 Seconds  
(without alignments)  
29.381 Million cell updates/sec

Title: US-09-846-033B-40  
Perfect score: 7  
Sequence: 1 ERGTLAR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7  
Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep:\*  
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4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4 US-09-731-558-18	Sequence 18, Appl
2	7	100.0	10	3 US-09-139-762A-73	Sequence 73, Appl
3	7	100.0	10	3 US-09-139-762A-84	Sequence 84, Appl
4	7	100.0	10	3 US-09-139-762A-99	Sequence 99, Appl
5	7	100.0	33	3 US-08-793-408-13	Sequence 13, Appl
6	7	100.0	33	3 US-09-139-762A-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1  
US-09-731-558-18  
; Sequence 18, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558  
; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06

; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SBS7  
; OTHER INFORMATION: recognition helix  
US-09-731-558-18

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ERGTLAR 7  
| | | | |  
Db 1 ERGTLAR 7

RESULT 2  
US-09-139-762A-73  
; Sequence 73, Application US/09139762A  
; Patent No. 6013453  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Sanchez Garcia, Isidro  
; TITLE OF INVENTION: Improvements in or Relating to  
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
; NUMBER OF SEQUENCES: 125  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/139,762A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/793,408  
; FILING DATE: 02-JUN-1997  
; APPLICATION NUMBER: PCT/GB95/01949  
; FILING DATE: 17-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9514598.1  
; FILING DATE: 18-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9422534.9  
; FILING DATE: 08-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9416880.4  
; FILING DATE: 20-AUG-1994  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-139-762A-73

Query Match 100.0%; Score 7; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERGTLAR 7  
| | | | |  
Db 1 ERGTLAR 7

RESULT 3  
US-09-139-762A-84  
; Sequence 84, Application US/09139762A  
; Patent No. 6013453  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Sanchez Garcia, Isidro  
; TITLE OF INVENTION: Improvements in or Relating to  
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
; NUMBER OF SEQUENCES: 125  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09139,762A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/793,408  
; FILING DATE: 02-JUN-1997  
; APPLICATION NUMBER: PCT/GB95/01949  
; FILING DATE: 17-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9514698.1  
; FILING DATE: 18-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9422534.9  
; FILING DATE: 08-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9416880.4  
; FILING DATE: 20-AUG-1994  
; INFORMATION FOR SEQ ID NO: 84:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-139-762A-84

Query Match 100.0%; Score 7; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERGTLAR 7  
| | | | |  
Db 1 ERGTLAR 7

RESULT 4  
US-09-139-762A-99  
; Sequence 99, Application US/09139762A  
; Patent No. 6013453  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Sanchez Garcia, Isidro

; TITLE OF INVENTION: Improvements in or Relating to  
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
; NUMBER OF SEQUENCES: 125  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09139,762A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/793,408  
; FILING DATE: 02-JUN-1997  
; APPLICATION NUMBER: PCT/GB95/01949  
; FILING DATE: 17-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9514698.1  
; FILING DATE: 18-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9422534.9  
; FILING DATE: 08-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9416880.4  
; FILING DATE: 20-AUG-1994  
; INFORMATION FOR SEQ ID NO: 99:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-139-762A-99

Query Match 100.0%; Score 7; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERGTLAR 7  
| | | | |  
Db 1 ERGTLAR 7

RESULT 5  
US-08-793-408-13  
; Sequence 13, Application US/08793408  
; Patent No. 6007988  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Sanchez Garcia, Isidro  
; TITLE OF INVENTION: Improvements in or Relating to  
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

Qy 1 ERGTLAR 7  
| | | | |  
Db 18 ERGTLAR 24

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-139-762A-13

Query Match          100.0%; Score 7; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. NO. 0.18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ERGTLAR 7
Db      18  ERGTLAR 24

Search completed: December 27, 2004, 18:12:04
Job time : 15.8 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:31 ; Search time 15.8 Seconds  
(without alignments)  
29.381 Million cell updates/sec

Title: US-09-846-033B-39

Perfect score: 7

Sequence: 1 DRSSLTR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*

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- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	10	3	US-09-139-762A-72 Sequence 72, Appl
2	7	100.0	10	3	US-09-139-762A-75 Sequence 75, Appl
3	7	100.0	10	3	US-09-139-762A-93 Sequence 93, Appl
4	7	100.0	27	4	US-09-424-487B-114 Sequence 114, Appl
5	7	100.0	28	4	US-09-424-487B-93 Sequence 9, Appl
6	7	100.0	28	4	US-09-424-487B-113 Sequence 113, Appl
7	7	100.0	33	3	US-08-793-408-12 Sequence 12, Appl
8	7	100.0	33	3	US-09-139-762A-12 Sequence 12, Appl
9	7	100.0	34	4	US-09-424-487B-112 Sequence 112, Appl
10	7	100.0	88	4	US-09-851-271A-2 Sequence 2, Appl
11	7	100.0	89	3	US-08-793-408-18 Sequence 18, Appl
12	7	100.0	89	3	US-09-139-762A-18 Sequence 18, Appl

#### ALIGNMENTS

RESULT 1  
US-09-139-762A-72  
; Sequence 72, Application US/09139762A  
; Patent No. 6013453  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Sanchez Garcia, Isidro  
; TITLE OF INVENTION: Improvements in or Relating to  
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA

NUMBER OF SEQUENCES: 125  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/139,762A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/793,408  
FILING DATE: 02-JUN-1997  
APPLICATION NUMBER: PCT/GB95/01949  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9514698.1  
FILING DATE: 18-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9422534.9  
FILING DATE: 08-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9416880.4  
FILING DATE: 20-AUG-1994  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-139-762A-72  
Query Match 100.0%; Score 7; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;  
QY 1 DRSSLTR 7  
Db 1 DRSSLTR 7  
RESULT 2  
US-09-139-762A-75  
; Sequence 75, Application US/09139762A  
; Patent No. 6013453  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Sanchez Garcia, Isidro  
; TITLE OF INVENTION: Improvements in or Relating to  
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
; NUMBER OF SEQUENCES: 125  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-139-762A-75

Query Match      100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DRSSLTR 7
Db      1 DRSSLTR 7

RESULT 3
US-09-139-762A-93
; Sequence 93, Application US/09139762A
; Patent No. 6013453
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Sanchez Garcia, Isidro
; TITLE OF INVENTION: Improvements in or Relating to
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-139-762A-93

Query Match      100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DRSSLTR 7
Db      1 DRSSLTR 7

RESULT 4
US-09-424-487B-114
; Sequence 114, Application US/09424487B
; Patent No. 6746838
; GENERAL INFORMATION:
; APPLICANT: CHOO, YEN
; APPLICANT: KLUG, AARON
; APPLICANT: ISALAN, MARK
; TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS
; FILE REFERENCE: 71278/264975
; CURRENT APPLICATION NUMBER: US/09/424,487B
; CURRENT FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: GB 9710809.6
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: PCT/GB98/01512
; PRIOR FILING DATE: 1998-05-26
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 114
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: peptide
US-09-424-487B-114

Query Match      100.0%; Score 7; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DRSSLTR 7
Db     12 DRSSLTR 18

RESULT 5
US-09-424-487B-9
; Sequence 9, Application US/09424487B
; Patent No. 6746838
; GENERAL INFORMATION:
; APPLICANT: CHOO, YEN
; APPLICANT: KLUG, AARON
; APPLICANT: ISALAN, MARK
; TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS
; FILE REFERENCE: 71278/264975
; CURRENT APPLICATION NUMBER: US/09/424,487B
; CURRENT FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: GB 9710809.6
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: PCT/GB98/01512
; PRIOR FILING DATE: 1998-05-26
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; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: peptide
US-09-424-487B-9

Query Match      100.0%; Score 7; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DRSSLTR 7
        |||||
Db      12 DRSSLTR 18

RESULT 6
US-09-424-487B-113
; Sequence 113, Application US/09424487B
; Patent No. 6746838
; GENERAL INFORMATION:
; APPLICANT: CHOO, YEN
; APPLICANT: KLUG, AARON
; APPLICANT: ISALAN, MARK
; TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS
; FILE REFERENCE: 71278/264975
; CURRENT APPLICATION NUMBER: US/09/424,487B
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: GB 9710809.6
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: PCT/GB98/01512
; PRIOR FILING DATE: 1998-05-26
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: peptide
US-09-424-487B-113

Query Match      100.0%; Score 7; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DRSSLTR 7
        |||||
Db      12 DRSSLTR 18

RESULT 7
US-08-793-408-12
; Sequence 12, Application US/08793408
; Patent No. 6007988
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Sanchez Garcia, Isidro
; TITLE OF INVENTION: Improvements in or Relating to
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: peptide
US-09-424-487B-9

Query Match      100.0%; Score 7; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DRSSLTR 7
        |||||
Db      12 DRSSLTR 18

RESULT 8
US-09-139-762A-12
; Sequence 12, Application US/09139762A
; Patent No. 6013453
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Sanchez Garcia, Isidro
; TITLE OF INVENTION: Improvements in or Relating to
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 114
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: peptide
US-09-424-487B-113

Query Match      100.0%; Score 7; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DRSSLTR 7
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Db      18 DRSSLTR 24
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; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,408
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-793-408-12

Query Match      100.0%; Score 7; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DRSSLTR 7
        |||||
Db      18 DRSSLTR 24

RESULT 8
US-09-139-762A-12
; Sequence 12, Application US/09139762A
; Patent No. 6013453
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Sanchez Garcia, Isidro
; TITLE OF INVENTION: Improvements in or Relating to
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: GB 9514698.1  
; FILING DATE: 18-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9422534.9  
; FILING DATE: 08-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9416880.4  
; FILING DATE: 20-AUG-1994  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-139-762A-12

Query Match 100.0%; Score 7; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.44;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRSSLTR 7  
Db 18 DRSSLTR 24

## RESULT 9

US-09-424-487B-112  
; Sequence 112, Application US/09424487B  
; Patent No. 6746838  
; GENERAL INFORMATION:  
; APPLICANT: CHOO, YEN  
; APPLICANT: KLUG, AARON  
; APPLICANT: ISALAN, MARK  
; TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS  
; FILE REFERENCE: 71278/264975  
; CURRENT APPLICATION NUMBER: US/09/424,487B  
; CURRENT FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: GB 9710809.6  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: PCT/GB98/01512  
; PRIOR FILING DATE: 1998-05-26  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 112  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger  
; OTHER INFORMATION: Peptide  
US-09-424-487B-112

Query Match 100.0%; Score 7; DB 4; Length 34;  
Best Local Similarity 100.0%; Pred. No. 0.45;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRSSLTR 7  
Db 18 DRSSLTR 24

## RESULT 10

US-09-851-271A-2  
; Sequence 2, Application US/09851271A  
; Patent No. 6733970  
; GENERAL INFORMATION:  
; APPLICANT: Gendex Limited  
; TITLE OF INVENTION: Screening System  
; FILE REFERENCE: 674538-2003  
; CURRENT APPLICATION NUMBER: US/09/851,271A  
; CURRENT FILING DATE: 2001-05-08  
; PRIOR APPLICATION NUMBER: PCT/GB99/03730

; PRIOR FILING DATE: 1999-11-09  
; PRIOR APPLICATION NUMBER: GB9824544.2  
; PRIOR FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 88  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: ZN\_FING  
; LOCATION: (1)..(88)  
; OTHER INFORMATION: protein sequence encoding a zinc-finger domain  
US-09-851-271A-2

Query Match 100.0%; Score 7; DB 4; Length 88;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRSSLTR 7  
Db 17 DRSSLTR 23

## RESULT 11

US-08-793-408-18  
; Sequence 18, Application US/08793408  
; Patent No. 6007988  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Sanchez Garcia, Isidro  
; TITLE OF INVENTION: Improvements in or Relating to  
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,408  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB95/01949  
; FILING DATE: 17-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9514698.1  
; FILING DATE: 18-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9422534.9  
; FILING DATE: 08-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9416880.4  
; FILING DATE: 20-AUG-1994  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 89 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: procein  
US-08-793-408-18

Query Match 100.0%; Score 7; DB 3; Length 89;

Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSSLTR 7  
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Db 18 DRSSLTR 24

RESULT 12  
US-09-139-762A-18  
; Sequence 18, Application US/09139762A  
; Patent No. 6013453  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Sanchez Garcia, Isidro  
; TITLE OF INVENTION: Improvements in or Relating to  
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
; NUMBER OF SEQUENCES: 125  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/139,762A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/793,408  
; FILING DATE: 02-JUN-1997  
; APPLICATION NUMBER: PCT/GB95/01949  
; FILING DATE: 17-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9514698.1  
; FILING DATE: 18-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9422534.9  
; FILING DATE: 08-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9416880.4  
; FILING DATE: 20-AUG-1994  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 89 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-09-139-762A-18

Query Match 100.0%; Score 7; DB 3; Length 89;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSSLTR 7  
| | | | |  
Db 18 DRSSLTR 24

Search completed: December 27, 2004, 18:12:04  
Job time : 15.8 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds  
(without alignments)  
29.289 Million cell updates/sec

Title: US-09-846-033B-94  
Perfect score: 7  
Sequence: 1 RSDHLTT 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 59

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pap:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	7	100.0	10	3	US-09-139-762A-19
3	7	100.0	10	3	US-09-139-762A-53
4	7	100.0	20	1	US-08-040-548-19
5	7	100.0	20	1	US-08-466-344-19
6	7	100.0	21	4	US-09-229-007A-95
7	7	100.0	21	4	US-10-113-424-95
8	7	100.0	26	2	US-08-620-151-111
9	7	100.0	28	1	US-08-040-548-34
10	7	100.0	28	1	US-08-466-344-34
11	7	100.0	28	3	US-09-058-459-1
12	7	100.0	28	3	US-09-127-926-1
13	7	100.0	28	3	US-09-037-179B-15
14	7	100.0	28	4	US-09-240-179-2
15	7	100.0	28	4	US-09-714-357-1
16	7	100.0	28	4	US-09-500-700-70
17	7	100.0	28	4	US-09-716-637-13
18	7	100.0	59	1	US-08-040-548-7
19	7	100.0	59	1	US-08-466-344-7
20	7	100.0	85	4	US-09-229-007A-8
21	7	100.0	85	4	US-10-113-424-8
22	7	100.0	86	6	5206152-3
23	7	100.0	87	4	US-10-057-552-1
24	7	100.0	89	1	US-08-040-548-8
25	7	100.0	89	1	US-08-466-344-8
26	7	100.0	91	3	US-08-863-813A-5
27	7	100.0	91	3	US-08-676-318A-5

28	7	100.0	91	4	US-09-500-700-5	Sequence 5, Appli
29	7	100.0	109	2	US-08-224-482-11	Sequence 11, Appl
30	7	100.0	153	3	US-08-863-813A-34	Sequence 34, Appl
31	7	100.0	153	3	US-08-863-813A-36	Sequence 36, Appl
32	7	100.0	153	3	US-08-676-318A-34	Sequence 34, Appl
33	7	100.0	153	3	US-08-676-318A-36	Sequence 36, Appl
34	7	100.0	153	4	US-09-500-700-34	Sequence 34, Appl
35	7	100.0	153	4	US-09-500-700-36	Sequence 36, Appl
36	7	100.0	181	3	US-08-863-813A-44	Sequence 44, Appl
37	7	100.0	181	3	US-08-676-318A-44	Sequence 44, Appl
38	7	100.0	181	4	US-09-500-700-44	Sequence 8, Appli
39	7	100.0	387	2	US-08-224-482-8	Sequence 1278, Ap
40	7	100.0	387	4	US-09-538-092-1278	Patent No. 5206152
41	7	100.0	453	6	5206152-7	Sequence 6, Appli
42	7	100.0	455	2	US-08-224-482-6	Sequence 2, Appli
43	7	100.0	456	1	US-08-040-548-2	Sequence 2, Appli
44	7	100.0	456	1	US-08-466-344-2	Sequence 66, Appl
45	7	100.0	456	4	US-09-919-039-66	

ALIGNMENTS

RESULT 1  
US-09-614-679A-19  
; Sequence 19, Application US/09614679A  
; Patent No. 6492117  
; GENERAL INFORMATION:  
; APPLICANT: CHOO, YEN  
; APPLICANT: ISALAN, MARK  
; APPLICANT: PATEL, SACHIN  
; APPLICANT: BALASUBRAMANIAN, SHANKAR  
; APPLICANT: LIU, XIAOHAI  
; TITLE OF INVENTION: MOLECULES  
; FILE REFERENCE: 71278/271599  
; CURRENT APPLICATION NUMBER: US/09/614,679A  
; CURRENT FILING DATE: 2000-07-12  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-614-679A-19

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7  
Db 1 RSDHLTT 7

RESULT 2  
US-09-139-762A-19  
; Sequence 19, Application US/09139762A  
; Patent No. 6013453  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Sanchez Garcia, Isidro  
; TITLE OF INVENTION: Improvements in or Relating to  
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
; NUMBER OF SEQUENCES: 125  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.





QY 1 RSDHLTT 7  
Db 9 RSDHLTT 15

RESULT 5  
US-08-466-344-19  
; Sequence 19, Application US/08466344  
; Patent No. 5773583  
; GENERAL INFORMATION:  
; APPLICANT: Sukhatne, Vikas P.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE  
; FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. 5773583th Clark Street, Suite 800  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,344  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/040,548  
; FILING DATE: 31-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coughlin, Daniel F.  
; REGISTRATION NUMBER: 36,111  
; REFERENCE/DOCKET NUMBER: arcd067  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 744-0090  
; TELEFAX: (312) 245-4961  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-466-344-19

Query Match 100.0%; Score 7; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.031; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 9 RSDHLTT 15

RESULT 6  
US-09-229-007A-95  
; Sequence 95, Application US/09229007A  
; Patent No. 6453242  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Case, Casey C.  
; APPLICANT: Cox III, George N.  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger  
; PROTEINS AND METHODS OF DESIGNING ZINC FINGER PROTEINS  
; TO BIND TO PRESELECTED SITES  
; NUMBER OF SEQUENCES: 136  
; CORRESPONDENCE ADDRESS:

Query Match 100.0%; Score 7; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.031; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 9 RSDHLTT 15

RESULT 7  
US-10-113-424-95  
; Sequence 95, Application US/10113424  
; Patent No. 6785613  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Case, Casey C.  
; APPLICANT: Cox III, George N.  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger  
; PROTEINS AND METHODS OF DESIGNING ZINC FINGER PROTEINS  
; TO BIND TO PRESELECTED SITES  
; NUMBER OF SEQUENCES: 136  
; CORRESPONDENCE ADDRESS:

Query Match 100.0%; Score 7; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.033; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 8 RSDHLTT 14

RESULT 8  
US-08-620-151-111  
; Sequence 111, Application US/08620151  
; Patent No. 5928955  
; GENERAL INFORMATION:  
; APPLICANT: Imperiali, Barbara  
; APPLICANT: Walkup, Grant K.  
; TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR  
; DIVALENT ZINC  
; NUMBER OF SEQUENCES: 136  
; CORRESPONDENCE ADDRESS:

Query Match 100.0%; Score 7; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.033; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 8 RSDHLTT 14

FILE REFERENCE: 019496-001800US  
; CURRENT APPLICATION NUMBER: US/09/229,007A  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 95  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence  
; OTHER INFORMATION: (F1, F2 and F3) from Zif 268  
US-09-229-007A-95

Query Match 100.0%; Score 7; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.033; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 8 RSDHLTT 14

FILE REFERENCE: 019496-001800US  
; CURRENT APPLICATION NUMBER: US/10/113,424  
; CURRENT FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 95  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence  
; OTHER INFORMATION: (F1, F2 and F3) from Zif 268  
US-10-113-424-95

Query Match 100.0%; Score 7; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.033; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 8 RSDHLTT 14

FILE REFERENCE: 019496-001800US  
; CURRENT APPLICATION NUMBER: US/09/229,007A  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 95  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence  
; OTHER INFORMATION: (F1, F2 and F3) from Zif 268  
US-10-113-424-95

Query Match 100.0%; Score 7; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.033; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 8 RSDHLTT 14

FILE REFERENCE: 019496-001800US  
; CURRENT APPLICATION NUMBER: US/10/113,424  
; CURRENT FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 95  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence  
; OTHER INFORMATION: (F1, F2 and F3) from Zif 268  
US-10-113-424-95

Query Match 100.0%; Score 7; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.033; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 8 RSDHLTT 14

ADDRESSEE: BRINKS, HOPER, GILSON & LIONE  
STREET: NBC Tower - Suite 3600, 455 N. Cityfront  
STREET: Plaza Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60611-5599  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,151  
FILING DATE: 22-MAR-1996  
CLASSIFICATION: 422  
ATTORNEY/AGENT INFORMATION:  
NAME: Shannon, Karen L.  
REGISTRATION NUMBER: 36,675  
REFERENCE/DOCKET NUMBER: 8597/6  
TELEPHONE: 312-321-4200  
TELEFAX: 312-321-4299  
INFORMATION FOR SEQ ID NO: 111:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-620-151-111

Query Match 100.0%; Score 7; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 13 RSDHLTT 19

RESULT 9  
US-08-040-548-34  
Sequence 34, Application US/08040548  
Patent No. 5763209  
GENERAL INFORMATION:  
APPLICANT: Sukhatme, Vikas P.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE  
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5763209th Clark Street, Suite 800  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/040,548  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coughlin, Daniel F.  
REGISTRATION NUMBER: 36,111  
REFERENCE/DOCKET NUMBER: arcd067  
TELEPHONE: (312) 744-0090  
TELEFAX: (312) 245-4961

INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-040-548-34

Query Match 100.0%; Score 7; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 9 RSDHLTT 15

RESULT 10  
US-08-466-344-34  
Sequence 34, Application US/08466344  
Patent No. 5773583  
GENERAL INFORMATION:  
APPLICANT: Sukhatme, Vikas P.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE  
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5773583th Clark Street, Suite 800  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,344  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION NUMBER: 08/040,548  
FILING DATE: 31-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coughlin, Daniel F.  
REGISTRATION NUMBER: 36,111  
REFERENCE/DOCKET NUMBER: arcd067  
TELEPHONE: (312) 744-0090  
TELEFAX: (312) 245-4961  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-466-344-34

Query Match 100.0%; Score 7; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 9 RSDHLTT 15

RESULT 11  
US-09-058-459-1

; Sequence 1, Application US/09058459

; Patent No. 6188965  
; GENERAL INFORMATION:  
; APPLICANT: Mayo, Stephen L.  
; APPLICANT: Dahiyat, Bassil I.  
; APPLICANT: Gordon, D. B.  
; APPLICANT: Street, Arthur  
; TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN  
; FILE REFERENCE: A65353-3/RFT/RMS/SJR  
; CURRENT APPLICATION NUMBER: US/09/058,459  
; CURRENT FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: 60/043,464  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/054,678  
; PRIOR FILING DATE: 1997-08-04  
; PRIOR APPLICATION NUMBER: 60/061,097  
; PRIOR FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Mouse  
; US-09-058-459-1

Query Match 100.0%; Score 7; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7  
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Db 14 RSDHLTT 20

RESULT 12

US-09-127-926-1  
; Sequence 1, Application US/09127926  
; Patent No. 6269312  
; GENERAL INFORMATION:  
; APPLICANT: Mayo, Stephen L.  
; APPLICANT: Dahiyat, Bassil I.  
; APPLICANT: Gordon, D. Benjamin  
; APPLICANT: Street, Arthur  
; APPLICANT: Su, Yaoying  
; TITLE OF INVENTION: Apparatus and Method for Automated Protein Design  
; FILE REFERENCE: A65353-4/RFT/RMS/SJR  
; CURRENT APPLICATION NUMBER: US/09/127,926  
; CURRENT FILING DATE: 1998-07-31  
; PRIOR APPLICATION NUMBER: 60/043,464  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/054,678  
; PRIOR FILING DATE: 1997-08-04  
; PRIOR APPLICATION NUMBER: 60/061,097  
; PRIOR FILING DATE: 1997-10-03  
; PRIOR APPLICATION NUMBER: 09/058,459  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: 60/087,561  
; PRIOR FILING DATE: 1998-06-01  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Mouse  
; US-09-127-926-1

Query Match 100.0%; Score 7; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7  
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Db 14 RSDHLTT 20

RESULT 13

US-09-037-179B-15  
; Sequence 15, Application US/09037179B  
; Patent No. 6316599  
; GENERAL INFORMATION:  
; APPLICANT: Call, Katherine M.  
; APPLICANT: Glaser, Thomas M.  
; APPLICANT: Ito, Caryn Y.  
; APPLICANT: Buckler, Alan J.  
; APPLICANT: Pelletier, Jerry  
; APPLICANT: Haber, Daniel A.  
; APPLICANT: Rose, Elise A.  
; APPLICANT: Housman, David E.  
; APPLICANT: Bruening, Wendy  
; APPLICANT: Darveau, Andre  
; TITLE OF INVENTION: Localization and Characterization of the  
; TITLE OF INVENTION: Wilms' Tumor Gene  
; FILE REFERENCE: 0050.1312-011  
; CURRENT APPLICATION NUMBER: US/09/037,179B  
; CURRENT FILING DATE: 1998-03-09  
; PRIOR APPLICATION NUMBER: US 08/102,942  
; PRIOR FILING DATE: 1993-08-02  
; PRIOR APPLICATION NUMBER: US 07/614,161  
; PRIOR FILING DATE: 1990-11-13  
; PRIOR APPLICATION NUMBER: US 07/435,780  
; PRIOR FILING DATE: 1989-11-13  
; PRIOR APPLICATION NUMBER: US 07/795,323  
; PRIOR FILING DATE: 1994-09-27  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Homo sapien  
; US-09-037-179B-15

Query Match 100.0%; Score 7; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7  
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Db 17 RSDHLTT 23

RESULT 14

US-09-240-179-2  
; Sequence 2, Application US/09240179  
; Patent No. 6410248  
; GENERAL INFORMATION:  
; APPLICANT: Graisman, Harvey A.  
; APPLICANT: Pabo, Carl O.  
; APPLICANT: Massachusetts Institute of Technology  
; TITLE OF INVENTION: A General Strategy for Selecting High-Affinity Zinc  
; TITLE OF INVENTION: Finger Proteins for Diverse DNA Target Sites  
; FILE REFERENCE: 019496-000220US  
; CURRENT APPLICATION NUMBER: US/09/240,179  
; CURRENT FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: US 60/073,223  
; EARLIER FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Zif268 zinc  
; OTHER INFORMATION: finger 2  
; US-09-240-179-2

Query Match 100.0%; Score 7; DB 4; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.043;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
 Db 13 RSDHLTT 19

RESULT 15  
 US-09-714-357-1  
 ; Sequence 1, Application US/09714357  
 ; Patent No. 6708120  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mayo, Stephen L.  
 ; APPLICANT: Dahiyat, Basil I.  
 ; APPLICANT: Gordon, D. B.  
 ; APPLICANT: Street, Arthur  
 ; TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN  
 ; FILE REFERENCE: A65353-3/RFT/RMS/SJR  
 ; CURRENT APPLICATION NUMBER: US/09/714,357  
 ; CURRENT FILING DATE: 2000-11-15  
 ; PRIOR APPLICATION NUMBER: 09/058,459  
 ; PRIOR FILING DATE: 1998-04-10  
 ; PRIOR APPLICATION NUMBER: 60/054,678  
 ; PRIOR FILING DATE: 1997-08-04  
 ; PRIOR APPLICATION NUMBER: 60/061,097  
 ; PRIOR FILING DATE: 1997-10-03  
 ; NUMBER OF SEQ ID NOS: 79  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 28  
 ; TYPE: PRT  
 ; ORGANISM: Mouse  
 US-09-714-357-1

Query Match 100.0%; Score 7; DB 4; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.043;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
 Db 14 RSDHLTT 20

Search completed: December 27, 2004, 20:31:04  
 Job time : 15.85 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds  
(without alignments)  
29.289 Million cell updates/sec

Title: US-09-846-033B-93  
Perfect score: 7  
Sequence: 1 RSDNLQ 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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No matches found

Search completed: December 27, 2004, 20:31:04  
Job time : 15.85 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds  
(without alignments)  
29.289 Million cell updates/sec

Title: US-09-846-033B-92  
Perfect score: 7  
Sequence: 1 QRAHLAR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCRUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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No matches found

Search completed: December 27, 2004, 20:31:04  
Job time : 15.85 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds  
(without alignments)  
29.289 Million cell updates/sec

Title: US-09-846-033B-91  
Perfect score: 7  
Sequence: 1 RSDHLSR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
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3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-14
2	7	100.0	7	4	US-09-779-233-44
3	7	100.0	7	4	US-09-716-637-29
4	7	100.0	99	4	US-09-229-037-15
5	7	100.0	99	4	US-09-478-681-15
6	7	100.0	99	4	US-09-779-233-3
7	7	100.0	196	4	US-09-229-037-30
8	7	100.0	196	4	US-09-478-681-30
9	7	100.0	196	4	US-09-779-233-18

ALIGNMENTS

RESULT 1  
US-09-731-558-14  
; Sequence 14, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731.558

; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; - OTHER INFORMATION: Description of Artificial Sequence:SBS3  
; - OTHER INFORMATION: recognition helix  
US-09-731-558-14

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
| | | | |  
Db 1 RSDHLSR 7

RESULT 2

US-09-779-233-44  
; Sequence 44, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; - OTHER INFORMATION: Description of Artificial Sequence: recognition  
; - OTHER INFORMATION: helix  
US-09-779-233-44

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
| | | | |  
Db 1 RSDHLSR 7

RESULT 3

US-09-716-637-29  
; Sequence 29, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29

Query Match          100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 1 RSDHLSR 7

RESULT 4
US-09-229-037-15
; Sequence 15, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-229-037-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 5
US-09-478-681-15
; Sequence 15, Application US/09478681
; Patent No. 6607882
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric E.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; FILE REFERENCE: 8325-0002.10 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/478,681
; CURRENT FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
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; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-478-681-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 6
US-09-779-233-3
; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 7
US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-229-037-30

Query Match          100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RSDHLSR 7  
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Db 178 RSDHLSR 184

RESULT 8  
US-09-478-681-30  
; Sequence 30, Application US/09478681  
; Patent No. 6607882  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:designed  
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpni to BamHI  
US-09-478-681-30

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
|||||||  
Db 178 RSDHLSR 184

RESULT 9  
US-09-779-233-18  
; Sequence 18, Application US/09779233  
; Patent No. 669558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1  
US-09-779-233-18

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
|||||||  
Db 178 RSDHLSR 184

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds  
(without alignments)  
29.289 Million cell updates/sec

Title: US-09-846-033B-90  
Perfect score: 7  
Sequence: 1 RSDNLR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-13 Sequence 13, Appl
2	7	100.0	7	4	US-09-779-233-43 Sequence 43, Appl

ALIGNMENTS

RESULT 1  
US-09-731-558-13  
; Sequence 13, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558  
; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 7

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:SBS2  
; OTHER INFORMATION: recognition helix  
US-09-731-558-13

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDNLR 7  
Db 1 RSDNLR 7  
|||||

RESULT 2  
US-09-779-233-43  
; Sequence 43, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
; OTHER INFORMATION: helix  
US-09-779-233-43

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDNLR 7  
Db 1 RSDNLR 7  
|||||

Search completed: December 27, 2004, 20:31:03  
Job time : 15.85 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds  
(without alignments)  
29.289 Million cell updates/sec

Title: US-09-846-033B-89  
Perfect score: 7  
Sequence: 1 RSDHLSK 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7  
Total number of hits satisfying chosen parameters: 24

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	12	4	US-09-995-973-37
2	7	100.0	21	4	US-09-229-007A-96
3	7	100.0	21	4	US-10-113-424-96
4	7	100.0	26	2	US-08-620-151-3
5	7	100.0	77	2	US-08-570-227A-5
6	7	100.0	77	2	US-08-570-227A-6
7	7	100.0	77	2	US-08-570-227A-7
8	7	100.0	77	3	US-09-077-991-7
9	7	100.0	77	3	US-09-077-991-8
10	7	100.0	77	3	US-09-077-991-9
11	7	100.0	94	4	US-09-229-007A-9
12	7	100.0	94	4	US-10-113-424-9
13	7	100.0	94	4	US-09-716-637-16
14	7	100.0	97	4	US-09-395-448-15
15	7	100.0	97	4	US-09-925-796-15
16	7	100.0	97	4	US-09-941-450-15
17	7	100.0	98	4	US-09-229-007A-10
18	7	100.0	98	4	US-10-113-424-10
19	7	100.0	100	4	US-09-716-637-18
20	7	100.0	168	2	US-08-353-476-73
21	7	100.0	241	2	US-08-353-476-116
22	7	100.0	273	2	US-08-353-476-112
23	7	100.0	784	4	US-09-538-092-1254
24	7	100.0	785	4	US-09-538-092-872

ALIGNMENTS

RESULT 1  
US-09-995-973-37  
; Sequence 37, Application US/09995973  
; Patent No. 6706470  
; GENERAL INFORMATION:  
; APPLICANT: CHOO, Yen  
; APPLICANT: ULLMAN, Christopher G.  
; TITLE OF INVENTION: GENE SWITCHES  
; FILE REFERENCE: 8325-2003 / G7-US1  
; CURRENT APPLICATION NUMBER: US/09/995, 973  
; CURRENT FILING DATE: 2002-03-19  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: zinc finger  
; OTHER INFORMATION: binding domain  
US-09-995-973-37

Query Match 100.0%; Score 7; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.039;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSK 7  
Db 1 RSDHLSK 7

RESULT 2  
US-09-229-007A-96  
; Sequence 96, Application US/09229007A  
; Patent No. 6453242  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Case, Casey C.  
; APPLICANT: Cox III, George N.  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger  
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins  
; TITLE OF INVENTION: to Bind to Preslected Sites  
; FILE REFERENCE: 019496-001800US  
; CURRENT APPLICATION NUMBER: US/09/229,007A  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 96  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence  
; OTHER INFORMATION: (F1, F2, F3) from SP1  
US-09-229-007A-96

Query Match 100.0%; Score 7; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.063;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSK 7  
Db 15 RSDHLSK 21

RESULT 3  
US-10-113-424-96  
; Sequence 96, Application US/10113424

; Patent No. 6785613  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Case, Casey C.  
; APPLICANT: Cox III, George N.  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger  
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins  
; TITLE OF INVENTION: to Bind to Preslected Sites  
; FILE REFERENCE: 019496-001800US  
; CURRENT APPLICATION NUMBER: US/10/113,424  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US/09/229,007A  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 96  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence  
; OTHER INFORMATION: (F1, F2, F3) from SP1  
US-10-113-424-96

Query Match 100.0%; Score 7; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.063; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSK 7  
Db 15 RSDHLSK 21

RESULT 4  
US-08-620-151-3  
; Sequence 3, Application US/08620151  
; Patent No. 5928955  
; GENERAL INFORMATION:  
; APPLICANT: Imperiali, Barbara  
; APPLICANT: Walkup, Grant K.  
; TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR  
; TITLE OF INVENTION: DIVALENT ZINC  
; NUMBER OF SEQUENCES: 136  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BRINKS, HOFER, GILSON & LIONE  
; STREET: NBC Tower - Suite 3600, 455 N. Cityfront  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60611-5599  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/620,151  
; FILING DATE: 22-MAR-1996  
; CLASSIFICATION: 422  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Shannon, Karen L.  
; REGISTRATION NUMBER: 36,675  
; REFERENCE/DOCKET NUMBER: 8597/6  
; TELEPHONE: 312-321-4200  
; TELEFAX: 312-321-4299  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids

; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-620-151-3  
Query Match 100.0%; Score 7; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.076; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSK 7  
Db 13 RSDHLSK 19

RESULT 5  
US-08-570-227A-5  
; Sequence 5, Application US/08570227A  
; Patent No. 5981217  
; GENERAL INFORMATION:  
; APPLICANT: Subramaniam, M.  
; APPLICANT: Speleberg, T. C.  
; TITLE OF INVENTION: DNA ENCODING TGF-BETA INDUCIBLE  
; TITLE OF INVENTION: EARLY FACTOR-1 (TIEF-1), A GENE EXPRESSED  
; TITLE OF INVENTION: BY OSTEOBLASTS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.  
; STREET: P.O. Box 2938  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/570,227A  
; FILING DATE: 11-DEC-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Woessner, Warren D.  
; REGISTRATION NUMBER: 30,440  
; REFERENCE/DOCKET NUMBER: 150.157US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-359-3260  
; TELEFAX: 612-359-3263  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 77 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-570-227A-5

Query Match 100.0%; Score 7; DB 2; Length 77;  
Best Local Similarity 100.0%; Pred. No. 0.19; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSK 7  
Db 70 RSDHLSK 76

RESULT 6  
US-08-570-227A-6



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; Sequence 6, Application US/08570227A
; Patent No. 5981217
; GENERAL INFORMATION:
; APPLICANT: Subramaniam, M.
; APPLICANT: Speisberg, T. C.
; TITLE OF INVENTION: DNA ENCODING TGF-BETA INDUCIBLE
; TITLE OF INVENTION: EARLY FACTOR-1 (TIEF-1), A GENE EXPRESSED
; TITLE OF INVENTION: BY OSTEOBLASTS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,227A
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 150.157US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-359-3260
; TELEFAX: 612-359-3263
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-570-227A-6

Query Match 100.0%; Score 7; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSK 7
Db 70 RSDHLSK 76

RESULT 7
US-08-570-227A-7
; Sequence 7, Application US/08570227A
; Patent No. 5981217
; GENERAL INFORMATION:
; APPLICANT: Subramaniam, M.
; APPLICANT: Speisberg, T. C.
; TITLE OF INVENTION: DNA ENCODING TGF-BETA INDUCIBLE
; TITLE OF INVENTION: EARLY FACTOR-1 (TIEF-1), A GENE EXPRESSED
; TITLE OF INVENTION: BY OSTEOBLASTS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,227A
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 150.157US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-359-3260
; TELEFAX: 612-359-3263
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-570-227A-7

Query Match 100.0%; Score 7; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSK 7
Db 70 RSDHLSK 76

RESULT 8
US-09-077-991-7
; Sequence 7, Application US/09077991
; Patent No. 6207175
; GENERAL INFORMATION:
; APPLICANT: Subramaniam, M.
; APPLICANT: Speisberg, T. C.
; APPLICANT: Roche, P. C.
; TITLE OF INVENTION: TGF-Beta inducible early factor-1
; TITLE OF INVENTION: (TIEF-1) and a method to detect breast cancer
; FILE REFERENCE: 150.157US2
; CURRENT APPLICATION NUMBER: US/09/077,991
; CURRENT FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: PCT/US96/19555
; EARLIER FILING DATE: 1996-12-11
; EARLIER APPLICATION NUMBER: US 08/570,227
; EARLIER FILING DATE: 1995-12-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-077-991-7

Query Match 100.0%; Score 7; DB 3; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSK 7
Db 70 RSDHLSK 76

RESULT 9
US-09-077-991-8
```

```
; Sequence 8, Application US/09077991
; Patent No. 6207375
; GENERAL INFORMATION:
; APPLICANT: Subramaniam, M.
; APPLICANT: Spelsberg, T.C.
; APPLICANT: Roche, P.C.
; TITLE OF INVENTION: TGF-Beta inducible early factor-1
; TITLE OF INVENTION: (TIEF-1) and a method to detect breast cancer
; FILE REFERENCE: 150.157US2
; CURRENT APPLICATION NUMBER: US/09/077,991
; CURRENT FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: PCT/US96/19555
; EARLIER FILING DATE: 1996-12-11
; EARLIER APPLICATION NUMBER: US 08/570,227
; EARLIER FILING DATE: 1995-12-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-077-991-8

Query Match      100.0%; Score 7; DB 3; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSK 7
Db 70 RSDHLSK 76

RESULT 10
US-09-077-991-9
; Sequence 9, Application US/09077991
; Patent No. 6207375
; GENERAL INFORMATION:
; APPLICANT: Subramaniam, M.
; APPLICANT: Spelsberg, T.C.
; APPLICANT: Roche, P.C.
; TITLE OF INVENTION: TGF-Beta inducible early factor-1
; TITLE OF INVENTION: (TIEF-1) and a method to detect breast cancer
; FILE REFERENCE: 150.157US2
; CURRENT APPLICATION NUMBER: US/09/077,991
; CURRENT FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: PCT/US96/19555
; EARLIER FILING DATE: 1996-12-11
; EARLIER APPLICATION NUMBER: US 08/570,227
; EARLIER FILING DATE: 1995-12-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-077-991-9

Query Match      100.0%; Score 7; DB 3; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSK 7
Db 70 RSDHLSK 76

RESULT 11
US-09-229-007A-9
; Sequence 9, Application US/09229007A
; Patent No. 6453242
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Case, Casey C.
; APPLICANT: Cox III, George N.
; APPLICANT: Jamieson, Andrew J.
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
; TITLE OF INVENTION: to Bind to Preselcted Sites
; FILE REFERENCE: 019496-001800US
; CURRENT APPLICATION NUMBER: US/09/229,007A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:amino acids
; OTHER INFORMATION: 531-624 in Sp-1 transcription factor
US-10-113-424-9

Query Match      100.0%; Score 7; DB 4; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSK 7
Db 78 RSDHLSK 84

RESULT 12
US-10-113-424-9
; Sequence 9, Application US/10113424
; Patent No. 6785613
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Case, Casey C.
; APPLICANT: Cox III, George N.
; APPLICANT: Jamieson, Andrew J.
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
; TITLE OF INVENTION: to Bind to Preselcted Sites
; FILE REFERENCE: 019496-001800US
; CURRENT APPLICATION NUMBER: US/10/113,424
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US/09/229,007A
; PRIOR FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:amino acids
; OTHER INFORMATION: 531-624 in Sp-1 transcription factor
US-10-113-424-9

Query Match      100.0%; Score 7; DB 4; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSK 7
Db 78 RSDHLSK 84

RESULT 13
US-09-716-637-16
; Sequence 16, Application US/09716637
; Patent No. 6794136
```

; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 94  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Sp-1 protein  
US-09-716-637-16

Query Match 100.0%; Score 7; DB 4; Length 94;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSK 7  
Db 78 RSDHLSK 84

RESULT 14  
US-09-395-448-15  
; Sequence 15, Application US/09395448  
; Patent No. 6599692  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey C.  
; APPLICANT: Zhang, Lei  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Functional Genomics Using Zinc Finger Proteins  
; FILE REFERENCE: 019496-002000US  
; CURRENT APPLICATION NUMBER: US/09/395,448  
; CURRENT FILING DATE: 1999-09-14  
; PRIOR APPLICATION NUMBER: 09/229,007  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 09/229,037  
; PRIOR FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 97  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: designed ZFP  
US-09-395-448-15

Query Match 100.0%; Score 7; DB 4; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSK 7  
Db 79 RSDHLSK 85

RESULT 15  
US-09-925-796-15  
; Sequence 15, Application US/09925796  
; Patent No. 6777185  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey C.  
; APPLICANT: Zhang, Lei  
; APPLICANT: Sangamo Biosciences, Inc.

; TITLE OF INVENTION: Functional Genomics Using Zinc Finger Proteins  
; FILE REFERENCE: 019496-002000US  
; CURRENT APPLICATION NUMBER: US/09/925,796  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/395,448  
; PRIOR FILING DATE: 1999-09-14  
; PRIOR APPLICATION NUMBER: 09/229,037  
; PRIOR FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 97  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: designed ZFP  
US-09-925-796-15

Query Match 100.0%; Score 7; DB 4; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSK 7  
Db 79 RSDHLSK 85

Search completed: December 27, 2004, 20:31:03  
Job time : 15.85 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds  
(without alignments)  
29.289 Million cell updates/sec

Title: US-09-846-033B-88  
Perfect score: 7  
Sequence: 1 RSDALTQ 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database :
- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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No matches found

Search completed: December 27, 2004, 20:31:03  
Job time : 15.85 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds  
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Title: US-09-846-033B-87  
Perfect score: 7  
Sequence: 1 QSSHLLAR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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No matches found

Search completed: December 27, 2004, 20:31:03  
Job time : 15.85 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds  
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29.289 Million cell updates/sec

Title: US-09-846-033B-86  
Perfect score: 7  
Sequence: 1 QSGHLQR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : Issued Patents AA:\*
- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-23
					Sequence 23, Appl

ALIGNMENTS

RESULT 1  
US-09-731-558-23  
; Sequence 23, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558  
; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 7  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:SBS12  
; OTHER INFORMATION: recognition helix  
US-09-731-558-23

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGHLQR 7  
Db 1 QSGHLQR 7

Search completed: December 27, 2004, 20:31:03  
Job time : 15.85 secs

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29.289 Million cell updates/sec

Title: US-09-846-033B-84  
Perfect score: 7  
Sequence: 1 MSHLSR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : Issued Patents\_AA:\*
- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
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No-matches found

Search completed: December 27, 2004, 20:31:02  
Job time : 15.85 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds  
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29.289 Million cell updates/sec

Title: US-09-846-033B-83

Perfect score: 7

Sequence: 1 RSDHLTR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pcp.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	3 US-09-173-941-69	Sequence 69, Appl
2	7	100.0	7	4 US-09-494-190-69	Sequence 69, Appl
3	7	100.0	21	4 US-09-229-007A-94	Sequence 94, Appl
4	7	100.0	21	4 US-10-113-424-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1  
US-09-173-941-69  
; Sequence 69, Application US/09173941  
; Patent No. 6140081  
; GENERAL INFORMATION:  
; APPLICANT: BARBAS, Carlos F.  
; TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN  
; FILE REFERENCE: NOV00815  
; CURRENT APPLICATION NUMBER: US/09/173.941  
; CURRENT FILING DATE: 1998-10-16  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 69  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide

; OTHER INFORMATION: codon binding sequence  
US-09-173-941-69

Query Match 100.0%; Score 7; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTR 7  
| | | | |  
Db 1 RSDHLTR 7

RESULT 2

US-09-494-190-69  
; Sequence 69, Application US/09494190  
; Patent No. 6610512  
; GENERAL INFORMATION:  
; APPLICANT: BARBAS, Carlos F.  
; TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN  
; FILE REFERENCE: TSRI 645.2  
; CURRENT APPLICATION NUMBER: US/09/494.190  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: EP/99/07742  
; PRIOR FILING DATE: 1999-10-14  
; PRIOR APPLICATION NUMBER: US 09/173.941  
; PRIOR FILING DATE: 1998-10-16  
; NUMBER OF SEQ ID NOS: 126  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 69  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:phage display  
; OTHER INFORMATION: selected and mutagenized  
US-09-494-190-69

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTR 7  
| | | | |  
Db 1 RSDHLTR 7

RESULT 3

US-09-229-007A-94  
; Sequence 94, Application US/09229007A  
; Patent No. 6453242  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Case, Casey C.  
; APPLICANT: Cox III, George N.  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger  
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins  
; TITLE OF INVENTION: to Bind to Presselected Sites  
; FILE REFERENCE: 019496-001800US  
; CURRENT APPLICATION NUMBER: US/09/229.007A  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 94  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence  
; OTHER INFORMATION: (F1, F2 and F3) from SBS design GR-223  
US-09-229-007A-94

Query Match 100.0%; Score 7; DB 4; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0.021;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTR 7  
 |||||  
 Db 8 RSDHLTR 14

RESULT 4  
 US-10-113-424-94  
 ; Sequence 94, Application US/10113424  
 ; Patent No. 6785613  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Eisenberg, Stephen P.  
 ; APPLICANT: Case, Casey C.  
 ; APPLICANT: Cox III, George N.  
 ; APPLICANT: Jamieson, Andrew  
 ; APPLICANT: Rebar, Edward J.  
 ; APPLICANT: Sangamo Biosciences, Inc.  
 ; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger  
 ; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins  
 ; TITLE OF INVENTION: to Bind to Preslected Sites  
 ; FILE REFERENCE: 019496-001800US  
 ; CURRENT APPLICATION NUMBER: US/10/113,424  
 ; CURRENT FILING DATE: 2002-03-28  
 ; PRIOR APPLICATION NUMBER: US/09/229,007A  
 ; PRIOR FILING DATE: 1999-01-12  
 ; NUMBER OF SEQ ID NOS: 97  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 94  
 ; LENGTH: 21  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:ZEP sequence  
 ; OTHER INFORMATION: (F1, F2 and F3) from SBS design GR-223  
 US-10-113-424-94

Query Match 100.0%; Score 7; DB 4; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0.021;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTR 7  
 |||||  
 Db 8 RSDHLTR 14

Search completed: December 27, 2004, 20:31:02  
 Job time : 15.85 secs

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(without alignments)  
29.289 Million cell updates/sec

Title: US-09-846-033B-81  
Perfect score: 7  
Sequence: 1 RSDHLTT 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 59

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:  
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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-614-679A-19
2	7	100.0	10	3	US-09-139-762A-19
3	7	100.0	10	3	US-09-139-762A-53
4	7	100.0	20	1	US-08-040-548-19
5	7	100.0	20	1	US-08-466-344-19
6	7	100.0	21	4	US-09-229-007A-95
7	7	100.0	21	4	US-10-113-424-95
8	7	100.0	26	2	US-08-620-151-111
9	7	100.0	28	1	US-08-040-548-34
10	7	100.0	28	1	US-08-466-344-34
11	7	100.0	28	3	US-09-058-459-1
12	7	100.0	28	3	US-09-127-926-1
13	7	100.0	28	3	US-09-037-179B-15
14	7	100.0	28	4	US-09-240-179-2
15	7	100.0	28	4	US-09-714-357-1
16	7	100.0	28	4	US-09-500-700-70
17	7	100.0	28	4	US-09-716-637-13
18	7	100.0	59	1	US-08-040-548-7
19	7	100.0	59	1	US-08-466-344-7
20	7	100.0	85	4	US-09-229-007A-8
21	7	100.0	85	4	US-10-113-424-8
22	7	100.0	86	6	5206152-3
23	7	100.0	87	4	US-10-057-552-1
24	7	100.0	89	1	US-08-040-548-8
25	7	100.0	89	1	US-08-466-344-8
26	7	100.0	91	3	US-08-863-813A-5
27	7	100.0	91	3	US-08-676-318A-5

28	7	100.0	91	4	US-09-500-700-5	Sequence 5, Appli
29	7	100.0	109	2	US-08-224-482-11	Sequence 11, Appl
30	7	100.0	153	3	US-08-863-813A-34	Sequence 34, Appl
31	7	100.0	153	3	US-08-863-813A-36	Sequence 36, Appl
32	7	100.0	153	3	US-08-676-318A-34	Sequence 34, Appl
33	7	100.0	153	3	US-08-676-318A-36	Sequence 36, Appl
34	7	100.0	153	4	US-09-500-700-34	Sequence 34, Appl
35	7	100.0	153	4	US-09-500-700-36	Sequence 36, Appl
36	7	100.0	181	3	US-08-863-813A-44	Sequence 44, Appl
37	7	100.0	181	3	US-08-676-318A-44	Sequence 44, Appl
38	7	100.0	181	4	US-09-500-700-44	Sequence 8, Appli
39	7	100.0	387	2	US-08-224-482-8	Sequence 1278, Ap
40	7	100.0	387	4	US-09-538-092-1278	Patent No. 5206152
41	7	100.0	453	6	5206152-7	Sequence 6, Appli
42	7	100.0	455	2	US-08-224-482-6	Sequence 2, Appli
43	7	100.0	456	1	US-08-040-548-2	Sequence 2, Appli
44	7	100.0	456	1	US-08-466-344-2	Sequence 66, Appl
45	7	100.0	456	4	US-09-919-039-66	

ALIGNMENTS

RESULT 1  
US-09-614-679A-19  
; Sequence 19, Application US/09614679A  
; Patent No. 6492117  
; GENERAL INFORMATION:  
; APPLICANT: CHOO, YEN  
; APPLICANT: ISALAN, MARK  
; APPLICANT: PATEL, SACHIN  
; APPLICANT: BALASUBRAMANIAN, SHANKAR  
; APPLICANT: LIU, XIAOHAI  
; TITLE OF INVENTION: MOLECULES  
; FILE REFERENCE: 71278/271599  
; CURRENT APPLICATION NUMBER: US/09/614,679A  
; CURRENT FILING DATE: 2000-07-12  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
; OTHER INFORMATION: peptide  
US-09-614-679A-19

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7  
Db 1 RSDHLTT 7

RESULT 2  
US-09-139-762A-19  
; Sequence 19, Application US/09139762A  
; Patent No. 6013453  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Sanchez Garcia, Isidro  
; TITLE OF INVENTION: Improvements in or Relating to  
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
; NUMBER OF SEQUENCES: 125  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.

```

; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-139-762A-19

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
Db 1 RSDHLTT 7

RESULT 3
US-09-139-762A-53
; Sequence 53, Application US/09139762A
; Patent No. 6013453
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; TITLE OF INVENTION: Improvements in or Relating to
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997
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; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-139-762A-53

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
Db 1 RSDHLTT 7

RESULT 4
US-08-040-548-19
; Sequence 19, Application US/08040548
; Patent No. 5763209
; GENERAL INFORMATION:
; APPLICANT: Sukhatme, Vikas P.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
; TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 NO. 5763209th Clark Street, Suite 800
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/040,548
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coughlin, Daniel F.
; REGISTRATION NUMBER: 36,111
; REFERENCE/DOCKET NUMBER: arcd067
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 744-0090
; TELEFAX: (312) 245-4961
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-040-548-19

Query Match 100.0%; Score 7; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RSDHLTT 7  
| | | | |  
Db 9 RSDHLTT 15

## RESULT 5

US-08-466-344-19  
; Sequence 19, Application US/08466344  
; Patent No. 5773583  
; GENERAL INFORMATION:  
; APPLICANT: Sukhame, Vikas P.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE  
; FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. 5773583th Clark Street, Suite 800  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,344  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/040,548  
; FILING DATE: 31-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coughlin, Daniel F.  
; REGISTRATION NUMBER: 36,111  
; REFERENCE/DOCKET NUMBER: arc0067  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 744-0090  
; TELEFAX: (312) 245-4961  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-466-344-19

Query Match 100.0%; Score 7; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.031;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
| | | | |  
Db 9 RSDHLTT 15

## RESULT 6

US-09-229-007A-95  
; Sequence 95, Application US/09229007A  
; Patent No. 6453242  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Case, Casey C.  
; APPLICANT: Cox III, George N.  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger  
; PROTEINS AND METHODS OF DESIGNING ZINC FINGER PROTEINS  
; TO BIND TO PRESELECTED SITES

; FILE REFERENCE: 019496-001800US  
; CURRENT APPLICATION NUMBER: US/09/229,007A  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 95  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence  
; OTHER INFORMATION: (F1, F2 and F3) from Zif 268  
US-09-229-007A-95

Query Match 100.0%; Score 7; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.033;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
| | | | |  
Db 8 RSDHLTT 14

## RESULT 7

US-10-113-424-95  
; Sequence 95, Application US/10113424  
; Patent No. 6785613  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Case, Casey C.  
; APPLICANT: Cox III, George N.  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger  
; PROTEINS AND METHODS OF DESIGNING ZINC FINGER PROTEINS  
; TO BIND TO PRESELECTED SITES  
; FILE REFERENCE: 019496-001800US  
; CURRENT APPLICATION NUMBER: US/10/113,424  
; CURRENT FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US/09/229,007A  
; PRIOR FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 95  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence  
; OTHER INFORMATION: (F1, F2 and F3) from Zif 268  
US-10-113-424-95

Query Match 100.0%; Score 7; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.033;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
| | | | |  
Db 8 RSDHLTT 14

## RESULT 8

US-08-620-151-111  
; Sequence 111, Application US/08620151  
; Patent No. 5928955  
; GENERAL INFORMATION:  
; APPLICANT: Imperiali, Barbara  
; APPLICANT: Walkup, Grant K.  
; TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR  
; DIVALENT ZINC  
; NUMBER OF SEQUENCES: 136  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: BRINKS, HOFER, GILSON & LIONE  
STREET: NBC Tower - Suite 3600, 455 N. Cityfront  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60611-5599  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,151  
FILING DATE: 22-MAR-1996  
CLASSIFICATION: 422  
ATTORNEY/AGENT INFORMATION:  
NAME: Shannon, Karen L.  
REGISTRATION NUMBER: 36,675  
REFERENCE/DOCKET NUMBER: 8597/6  
TELEPHONE: 312-321-4200  
TELEFAX: 312-321-4299  
INFORMATION FOR SEQ ID NO: 111:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-620-151-111

Query Match 100.0%; Score 7; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7  
Db 13 RSDHLTT 19

RESULT 9  
US-08-040-548-34  
Sequence 34, Application US/08040548  
Patent No. 5763209  
GENERAL INFORMATION:  
APPLICANT: Sukhatme, Vikas P.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE  
FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5763209th Clark Street, Suite 800  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/040,548  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coughlin, Daniel F.  
REGISTRATION NUMBER: 36,111  
REFERENCE/DOCKET NUMBER: arcd067  
TELEPHONE: (312) 744-0090  
TELEFAX: (312) 245-4961

INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-040-548-34

Query Match 100.0%; Score 7; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7  
Db 9 RSDHLTT 15

RESULT 10  
US-08-466-344-34  
Sequence 34, Application US/08466344  
Patent No. 5773583  
GENERAL INFORMATION:  
APPLICANT: Sukhatme, Vikas P.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE  
FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5773583th Clark Street, Suite 800  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,344  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/040,548  
FILING DATE: 31-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coughlin, Daniel F.  
REGISTRATION NUMBER: 36,111  
REFERENCE/DOCKET NUMBER: arcd067  
TELEPHONE: (312) 744-0090  
TELEFAX: (312) 245-4961  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-466-344-34

Query Match 100.0%; Score 7; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7  
Db 9 RSDHLTT 15

RESULT 11  
US-09-058-459-1

; Sequence 1, Application US/09058459  
; Patent No. 6188965  
; GENERAL INFORMATION:  
; APPLICANT: Mayo, Stephen L. I.  
; APPLICANT: Dahiyat, Bassil I.  
; APPLICANT: Gordon, D. B.  
; APPLICANT: Street, Arthur  
; TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN  
; FILE REFERENCE: A65353-3/RFT/RMS/SJR  
; CURRENT APPLICATION NUMBER: US/09/058,459  
; CURRENT FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: 60/043,464  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/054,678  
; PRIOR FILING DATE: 1997-08-04  
; PRIOR APPLICATION NUMBER: 60/061,097  
; PRIOR FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-058-459-1

Query Match 100.0%; Score 7; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 14 RSDHLTT 20  
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## RESULT 12

US-09-127-926-1  
; Sequence 1, Application US/09127926  
; Patent No. 6269312  
; GENERAL INFORMATION:  
; APPLICANT: Mayo, Stephen L.  
; APPLICANT: Dahiyat, Bassil I.  
; APPLICANT: Gordon, D. Benjamin  
; APPLICANT: Street, Arthur  
; APPLICANT: Su, Yaoying  
; TITLE OF INVENTION: Apparatus and Method for Automated Protein Design  
; FILE REFERENCE: A65353-4/RFT/RMS/SJR  
; CURRENT APPLICATION NUMBER: US/09/127,926  
; CURRENT FILING DATE: 1998-07-31  
; PRIOR APPLICATION NUMBER: 60/043,464  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/054,678  
; PRIOR FILING DATE: 1997-08-04  
; PRIOR APPLICATION NUMBER: 60/061,097  
; PRIOR FILING DATE: 1997-10-03  
; PRIOR APPLICATION NUMBER: 09/058,459  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: 60/087,561  
; PRIOR FILING DATE: 1998-06-01  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-127-926-1

Query Match 100.0%; Score 7; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 14 RSDHLTT 20  
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## RESULT 13

US-09-037-179B-15  
; Sequence 15, Application US/09037179B  
; Patent No. 6316599  
; GENERAL INFORMATION:  
; APPLICANT: Call, Katherine M.  
; APPLICANT: Glaser, Thomas M.  
; APPLICANT: Ito, Caryn Y.  
; APPLICANT: Buckler, Alan J.  
; APPLICANT: Pelletier, Jerry  
; APPLICANT: Haber, Daniel A.  
; APPLICANT: Rose, Elise A.  
; APPLICANT: Housman, David E.  
; APPLICANT: Bruening, Wendy  
; APPLICANT: Darveau, Andre  
; TITLE OF INVENTION: Localization and Characterization of the  
; FILE REFERENCE: 0050.1312-011  
; CURRENT APPLICATION NUMBER: US/09/037,179B  
; CURRENT FILING DATE: 1998-03-09  
; PRIOR APPLICATION NUMBER: US 08/102,942  
; PRIOR FILING DATE: 1993-08-02  
; PRIOR APPLICATION NUMBER: US 07/614,161  
; PRIOR FILING DATE: 1990-11-13  
; PRIOR APPLICATION NUMBER: US 07/435,780  
; PRIOR FILING DATE: 1989-11-13  
; PRIOR APPLICATION NUMBER: US 07/795,323  
; PRIOR FILING DATE: 1994-09-27  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-037-179B-15

Query Match 100.0%; Score 7; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 17 RSDHLTT 23  
|||||

## RESULT 14

US-09-240-179-2  
; Sequence 2, Application US/09240179  
; Patent No. 6410248  
; GENERAL INFORMATION:  
; APPLICANT: Greisman, Harvey A.  
; APPLICANT: Pabo, Carl O.  
; APPLICANT: Massachusetts Institute of Technology  
; TITLE OF INVENTION: A General Strategy for Selecting High-Affinity Zinc  
; FILE REFERENCE: 019496-000220US  
; CURRENT APPLICATION NUMBER: US/09/240,179  
; CURRENT FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: US 60/073,223  
; EARLIER FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Zif268 zinc  
US-09-240-179-2

Query Match 100.0%; Score 7; DB 4; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 13 RSDHLTT 19

RESULT 15  
US-09-714-357-1  
; Sequence 1, Application US/09714357  
; Patent No. 6708120  
; GENERAL INFORMATION:  
; APPLICANT: Mayo, Stephen L.  
; APPLICANT: Dahiyat, Bassil I.  
; APPLICANT: Gordon, D. B.  
; APPLICANT: Street, Arthur  
; TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN  
; FILE REFERENCE: A65353-3/RPT/RMS/SJR  
; CURRENT APPLICATION NUMBER: US/09/714,357  
; CURRENT FILING DATE: 2000-11-15  
; PRIOR APPLICATION NUMBER: 09/058,459  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: 60/054,678  
; PRIOR FILING DATE: 1997-08-04  
; PRIOR APPLICATION NUMBER: 60/061,097  
; PRIOR FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-714-357-1

Query Match 100.0%; Score 7; DB 4; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 14 RSDHLTT 20

Search completed: December 27, 2004, 20:31:02  
Job time : 15.85 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds  
(without alignments)  
29.289 Million cell updates/sec

Title: US-09-846-033B-80  
Perfect score: 7  
Sequence: 1 DRSHLAR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents\_AA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-22
					Sequence 22, Appl

ALIGNMENTS

RESULT 1  
US-09-731-558-22  
; Sequence 22, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558  
; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SEQ ID NO 22  
; SOFTWARE: PatentIn Ver. 2.1  
; LENGTH: 7  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:SBS11  
; OTHER INFORMATION: recognition helix  
US-09-731-558-22

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRSHLAR 7  
Db 1 DRSHLAR 7

Search completed: December 27, 2004, 20:31:02  
Job time : 16.85 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 18:12:11 ; Search time 15.9 Seconds  
(without alignments)  
29.197 Million cell updates/sec

Title: US-09-846-033B-77  
Perfect score: 7  
Sequence: 1 RSDNLQR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
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4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-716-637-30 Sequence 30, Appl

ALIGNMENTS

RESULT 1  
US-09-716-637-30  
; Sequence 30, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716.637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: VEGF-II P2  
US-09-716-637-30

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDNLQR 7  
|||  
Db 1 RSDNLQR 7

Search completed: December 27, 2004, 19:21:33  
Job time : 24.9 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 18:12:11 ; Search time 15.9 Seconds  
(without alignments)  
29.197 Million cell updates/sec

Title: US-09-846-033B-76  
Perfect score: 7  
Sequence: 1 RSDNLQR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
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3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OTHER INFORMATION: Description of Artificial Sequence: VEGF-II F2  
US-09-716-637-30

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDNLQR 7  
| | | | |  
Db 1 RSDNLQR 7

Search completed: December 27, 2004, 19:21:24  
Job time : 15.9 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-716-637-30 Sequence 30, Appl

RESULT 1  
US-09-716-637-30  
; Sequence 30, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716.637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-716-637-30 Sequence 30, Appl

SUMMARIES

ALIGNMENTS

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OM protein - protein search, using sw model

Run on: December 27, 2004, 18:12:11 ; Search time 15.9 seconds  
(without alignments)  
29.197 Million cell updates/sec

Title: US-09-846-033B-75  
Perfect score: 7  
Sequence: 1 RSDNLQR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : Issued Patents AA:\*
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  - 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-716-637-30 Sequence 30, Appl

ALIGNMENTS

RESULT 1  
US-09-716-637-30  
; Sequence 30, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: VEGF-II P2  
US-09-716-637-30

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDNLQR 7  
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Db 1 RSDNLQR 7

Search completed: December 27, 2004, 19:21:24  
Job time : 15.9 secs

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Qy 1 RSDHLSR 7  
|||||||  
Db 178 RSDHLSR 184

RESULT 8  
US-09-478-681-30  
; Sequence 30, Application US/09478681  
; Patent No. 6607882  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:designed  
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpnl to BamHI  
US-09-478-681-30

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSR 7  
|||||||  
Db 178 RSDHLSR 184

RESULT 9  
US-09-779-233-18  
; Sequence 18, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1  
US-09-779-233-18

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSR 7  
|||||||  
Db 178 RSDHLSR 184

Search completed: December 27, 2004, 21:40:39  
Job time : 16.35 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 19:43:18 ; Search time 52.7 Seconds  
(without alignments)  
47.701 Million cell updates/sec

Title: US-09-846-033B-109

Perfect score: 7

Sequence: 1 RSDHLSR 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1595201 seqs, 359116952 residues

Word size : 7

Total number of hits satisfying chosen parameters: 424

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:\*

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- 5: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/prodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/prodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/prodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/prodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/prodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	7	100.0	7	9	US-09-989-789-229
3	7	100.0	7	9	US-09-989-789-230
4	7	100.0	7	9	US-09-989-789-234
5	7	100.0	7	9	US-09-989-789-238
6	7	100.0	7	9	US-09-989-789-239
7	7	100.0	7	9	US-09-989-789-244
8	7	100.0	7	9	US-09-989-789-420
9	7	100.0	7	9	US-09-989-789-425
10	7	100.0	7	9	US-09-989-789-426
11	7	100.0	7	9	US-09-989-789-428
12	7	100.0	7	9	US-09-989-789-434
13	7	100.0	7	9	US-09-989-789-832

Sequence 840, App  
Sequence 888, App  
Sequence 1001, App  
Sequence 1089, App  
Sequence 1090, App  
Sequence 1091, App  
Sequence 1094, App  
Sequence 1138, App  
Sequence 1139, App  
Sequence 1178, App  
Sequence 1179, App  
Sequence 1199, App  
Sequence 1207, App  
Sequence 1219, App  
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Sequence 1717, App  
Sequence 1718, App

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7 100.0 US-09-989-789-1717  
7 100.0 US-09-989-789-1718

#### ALIGNMENTS

##### RESULT 1

US-09-779-233-44  
; Sequence 44, Application US/09779233  
; Patent No. US20020045158A1  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
; OTHER INFORMATION: helix  
US-09-779-233-44

Query Match 100.0%; Score 7; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSR 7  
Db 1 RSDHLSR 7

##### RESULT 2

US-09-989-789-229  
; Sequence 229, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang

```
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 229
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-229
```

```
Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RSDHLSR 7
        |||||||
Db      1 RSDHLSR 7
```

## RESULT 3

```
US-09-989-789-230
; Sequence 230, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 230
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-230
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```
Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RSDHLSR 7
        |||||||
Db      1 RSDHLSR 7
```

## RESULT 4

```
US-09-989-789-234
; Sequence 234, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 234
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
```

## US-09-989-789-234

```
Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RSDHLSR 7
        |||||||
Db      1 RSDHLSR 7
```

## RESULT 5

```
US-09-989-789-238
; Sequence 238, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 238
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-238
```

```
Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RSDHLSR 7
        |||||||
Db      1 RSDHLSR 7
```

## RESULT 6

```
US-09-989-789-239
; Sequence 239, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 239
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-239
```

```
Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RSDHLSR 7
        |||||||
Db      1 RSDHLSR 7
```

## RESULT 7

```
US-09-989-789-244
```



```
; Sequence 244, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 244
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-244

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLSR 7
        |||||
Db      1 RSDHLSR 7

RESULT 8
US-09-989-789-420
; Sequence 420, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 420
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-420

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLSR 7
        |||||
Db      1 RSDHLSR 7

RESULT 10
US-09-989-789-426
; Sequence 426, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 426
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-426

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLSR 7
        |||||
Db      1 RSDHLSR 7

RESULT 11
US-09-989-789-428
; Sequence 428, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 428
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-428

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLSR 7
        |||||
Db      1 RSDHLSR 7

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLSR 7
        |||||
Db      1 RSDHLSR 7

RESULT 9
US-09-989-789-425
; Sequence 425, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 425
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-425

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLSR 7
        |||||
Db      1 RSDHLSR 7

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLSR 7
        |||||
Db      1 RSDHLSR 7
```

```
RESULT 12
US-09-989-789-434
; Sequence 434, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 434
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-434
Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RSDHLSR 7
Db      1 RSDHLSR 7

RESULT 13
US-09-989-789-832
; Sequence 832, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 832
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-832
Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RSDHLSR 7
Db      1 RSDHLSR 7

RESULT 14
US-09-989-789-840
; Sequence 840, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
```

```
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 840
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-840
Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RSDHLSR 7
Db      1 RSDHLSR 7

RESULT 15
US-09-989-789-888
; Sequence 888, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 888
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-888
Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RSDHLSR 7
Db      1 RSDHLSR 7

Search completed: December 27, 2004, 20:52:54
Job time : 52.7 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 Seconds  
(without alignments)  
28.393 Million cell updates/sec

Title: US-09-846-033B-101  
Perfect score: 7  
Sequence: 1 RSDHLSR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-14
2	7	100.0	7	4	US-09-779-233-44
3	7	100.0	7	4	US-09-716-637-29
4	7	100.0	99	4	US-09-229-037-15
5	7	100.0	99	4	US-09-478-681-15
6	7	100.0	99	4	US-09-779-233-3
7	7	100.0	196	4	US-09-229-037-30
8	7	100.0	196	4	US-09-478-681-30
9	7	100.0	196	4	US-09-779-233-18

ALIGNMENTS

RESULT 1  
US-09-731-558-14  
; Sequence 14, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Casey, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731.558

; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:3BS3  
; OTHER INFORMATION: recognition helix  
US-09-731-558-14

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
| | | | |  
Db 1 RSDHLSR 7

RESULT 2

US-09-779-233-44  
; Sequence 44, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Casey, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
; OTHER INFORMATION: helix  
US-09-779-233-44

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
| | | | |  
Db 1 RSDHLSR 7

RESULT 3

US-09-716-637-29  
; Sequence 29, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: Liu, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29

Query Match          100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
   |||||
Db 1 RSDHLSR 7

RESULT 4
US-09-229-037-15
; Sequence 15, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-229-037-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
   |||||
Db 81 RSDHLSR 87

RESULT 5
US-09-478-681-15
; Sequence 15, Application US/09478681
; Patent No. 6607882
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric E.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS
; FILE REFERENCE: 8325-0002.10 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/478,681
; CURRENT FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
US-09-478-681-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
   |||||
Db 81 RSDHLSR 87

RESULT 6
US-09-779-233-3
; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
   |||||
Db 81 RSDHLSR 87

RESULT 7
US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-229-037-30

Query Match          100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 RSDHLSR 7  
|||||  
Db 178 RSDHLSR 184

## RESULT 8

US-09-478-681-30  
; Sequence 30, Application US/09478681  
; Patent No. 6607882  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:designed  
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpni to BamHI  
US-09-478-681-30

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
|||||  
Db 178 RSDHLSR 184

## RESULT 9

US-09-779-233-18  
; Sequence 18, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1  
US-09-779-233-18

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
|||||  
Db 178 RSDHLSR 184

Search completed: December 27, 2004, 21:40:38  
Job time : 16.35 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 Seconds  
(without alignments)  
28.393 Million cell updates/sec

Title: US-09-846-033B-112  
Perfect score: 7  
Sequence: 1 QSSDLTR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
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3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-17
2	7	100.0	7	4	US-09-779-233-37

ALIGNMENTS

RESULT 1  
US-09-731-558-17  
; Sequence 17, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731.558  
; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 7

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:8BS6  
; OTHER INFORMATION: recognition helix  
US-09-731-558-17

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSDLTR 7  
Db 1 QSSDLTR 7

RESULT 2

US-09-779-233-37  
; Sequence 37, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: linker  
US-09-779-233-37

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSDLTR 7  
Db 1 QSSDLTR 7

Search completed: December 27, 2004, 21:40:39  
Job time : 16.35 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 Seconds  
(without alignments)  
28.393 Million cell updates/sec

Title: US-09-846-033B-111  
Sequence: 1 RSDHLSR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-14
2	7	100.0	7	4	US-09-779-233-44
3	7	100.0	7	4	US-09-716-637-29
4	7	100.0	99	4	US-09-229-037-15
5	7	100.0	99	4	US-09-478-681-15
6	7	100.0	99	4	US-09-779-233-3
7	7	100.0	196	4	US-09-229-037-30
8	7	100.0	196	4	US-09-478-681-30
9	7	100.0	196	4	US-09-779-233-18

ALIGNMENTS

RESULT 1  
US-09-731-558-14  
; Sequence 14, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731.558

; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:SB53  
; OTHER INFORMATION: recognition helix  
US-09-731-558-14

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
| | | | |  
Db 1 RSDHLSR 7

RESULT 2

US-09-779-233-44  
; Sequence 44, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
; OTHER INFORMATION: helix  
US-09-779-233-44

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
| | | | |  
Db 1 RSDHLSR 7

RESULT 3

US-09-716-637-29  
; Sequence 29, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29

Query Match      100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 1 RSDHLSR 7
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RESULT 4
US-09-229-037-15
; Sequence 15, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-229-037-15

Query Match      100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87
|||||

RESULT 5
US-09-478-681-15
; Sequence 15, Application US/09478681
; Patent No. 6607882
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric E.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS
; FILE REFERENCE: 8325-0002.10 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/478,681
; CURRENT FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
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; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-478-681-15

Query Match      100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87
|||||

RESULT 6
US-09-779-233-3
; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3

Query Match      100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87
|||||

RESULT 7
US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpn1 to BamHI
US-09-229-037-30

Query Match      100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RSDHLSR 7  
|||||||  
Db 178 RSDHLSR 184

RESULT 8  
US-09-478-681-30  
; Sequence 30, Application US/09478681  
; Patent No. 6607882  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:designed  
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI  
US-09-478-681-30

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
|||||||  
Db 178 RSDHLSR 184

RESULT 9  
US-09-779-233-18  
; Sequence 18, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1  
US-09-779-233-18

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
|||||||  
Db 178 RSDHLSR 184

Search completed: December 27, 2004, 21:40:39  
Job time : 16.35 secs

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OM protein - protein search, using sw model

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(without alignments)  
28.393 Million cell updates/sec

Title: US-09-846-033B-110  
Perfect score: 7  
Sequence: 1 RSDALAR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6S COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	881	3 US-09-413-814-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1  
US-09-413-814-44  
; Sequence 44, Application US/09413814  
; Patent No. 6225064  
; GENERAL INFORMATION:  
; APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH  
; APPLICANT: Bristol-Myers Squibb, Co.  
; APPLICANT: Beyer, Stefan  
; APPLICANT: Bloecker, Helmut  
; APPLICANT: Brandt, Petra  
; APPLICANT: Cino, Paul W  
; APPLICANT: Dougherty, Brian A  
; APPLICANT: Goldberg, Steven L  
; APPLICANT: Hofle, Gerhard  
; APPLICANT: Mueller, Joachim  
; APPLICANT: Reichenbach, Hans  
; TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or  
; TITLE OF INVENTION: heteropolymers of polyketide compounds  
; FILE REFERENCE: PCT/US 99/23535  
; CURRENT APPLICATION NUMBER: US/09/413,814  
; CURRENT FILING DATE: 1999-10-07

; EARLIER APPLICATION NUMBER: DE 198 46 493.2  
; EARLIER FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 44  
; LENGTH: 881  
; TYPE: PRT  
; ORGANISM: Sorangium cellulosum  
US-09-413-814-44

Query Match 100.0%; Score 7; DB 3; Length 881;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDALAR 7  
|||  
Db 295 RSDALAR 301

Search completed: December 27, 2004, 21:40:39  
Job time : 16.35 secs

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OM protein - protein search, using sw model

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(without alignments)  
28.393 Million cell updates/sec

Title: US-09-846-033B-109  
Perfect score: 7  
Sequence: 1 RSDHLSR 7

Scoring table: OLIGO  
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Searched: 478139 seqs, 66318000 residues

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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfilee1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-14
2	7	100.0	7	4	US-09-779-233-44
3	7	100.0	7	4	US-09-716-637-29
4	7	100.0	99	4	US-09-229-037-15
5	7	100.0	99	4	US-09-478-681-15
6	7	100.0	99	4	US-09-779-233-3
7	7	100.0	196	4	US-09-229-037-30
8	7	100.0	196	4	US-09-478-681-30
9	7	100.0	196	4	US-09-779-233-18

#### ALIGNMENTS

RESULT 1  
US-09-731-558-14  
; Sequence 14, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558

; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SBS3  
; OTHER INFORMATION: recognition helix  
US-09-731-558-14

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
Db 1 RSDHLSR 7

#### RESULT 2

US-09-779-233-44  
; Sequence 44, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
; OTHER INFORMATION: helix  
US-09-779-233-44

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
Db 1 RSDHLSR 7

#### RESULT 3

US-09-716-637-29  
; Sequence 29, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29

Query Match          100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
DB 1 RSDHLSR 7

RESULT 4
US-09-229-037-15
; Sequence 15, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-229-037-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
DB 81 RSDHLSR 87

RESULT 5
US-09-478-681-15
; Sequence 15, Application US/09478681
; Patent No. 6607882
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric E.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS
; FILE REFERENCE: 8325-0002.10 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/478,681
; CURRENT FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
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; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-478-681-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
DB 81 RSDHLSR 87

RESULT 6
US-09-779-233-3
; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
DB 81 RSDHLSR 87

RESULT 7
US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-229-037-30

Query Match          100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:31 ; Search time 15.8 Seconds  
(without alignments)  
29.381 Million cell updates/sec

Title: US-09-846-033B-31  
Perfect score: 7  
Sequence: 1 RSDHLTT 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 59

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
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5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfilee1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-614-679A-19
2	7	100.0	10	3	US-09-139-762A-19
3	7	100.0	10	3	US-09-139-762A-53
4	7	100.0	20	1	US-08-040-548-19
5	7	100.0	20	1	US-08-466-344-19
6	7	100.0	21	4	US-09-229-007A-95
7	7	100.0	21	4	US-10-113-424-95
8	7	100.0	26	2	US-08-620-151-111
9	7	100.0	28	1	US-08-040-548-34
10	7	100.0	28	1	US-08-466-344-34
11	7	100.0	28	3	US-09-058-459-1
12	7	100.0	28	3	US-09-127-926-1
13	7	100.0	28	3	US-09-037-179B-15
14	7	100.0	28	4	US-09-240-179-2
15	7	100.0	28	4	US-09-714-357-1
16	7	100.0	28	4	US-09-500-700-70
17	7	100.0	28	4	US-09-716-637-13
18	7	100.0	59	1	US-08-040-548-7
19	7	100.0	59	1	US-08-466-344-7
20	7	100.0	85	4	US-09-229-007A-8
21	7	100.0	85	4	US-10-113-424-8
22	7	100.0	85	6	5206152-3
23	7	100.0	87	4	US-10-057-552-1
24	7	100.0	89	1	US-08-040-548-8
25	7	100.0	89	1	US-08-466-344-8
26	7	100.0	91	3	US-08-863-813A-5
27	7	100.0	91	3	US-08-676-318A-5

28	7	100.0	91	4	US-09-500-700-5	Sequence 5, Appli
29	7	100.0	109	2	US-08-224-482-11	Sequence 11, Appl
30	7	100.0	153	3	US-08-863-813A-34	Sequence 34, Appl
31	7	100.0	153	3	US-08-863-813A-36	Sequence 36, Appl
32	7	100.0	153	3	US-08-676-318A-34	Sequence 34, Appl
33	7	100.0	153	3	US-08-676-318A-36	Sequence 36, Appl
34	7	100.0	153	4	US-09-500-700-34	Sequence 34, Appl
35	7	100.0	153	4	US-09-500-700-36	Sequence 36, Appl
36	7	100.0	181	3	US-08-863-813A-44	Sequence 44, Appl
37	7	100.0	181	3	US-08-676-318A-44	Sequence 44, Appl
38	7	100.0	181	4	US-09-500-700-44	Sequence 44, Appl
39	7	100.0	387	2	US-08-224-482-8	Sequence 8, Appli
40	7	100.0	387	2	US-09-538-092-1278	Sequence 1278, Ap
41	7	100.0	453	6	5206152-7	Patent No. 5206152
42	7	100.0	455	2	US-08-224-482-6	Sequence 6, Appli
43	7	100.0	456	1	US-08-040-548-2	Sequence 2, Appli
44	7	100.0	456	1	US-08-466-344-2	Sequence 2, Appli
45	7	100.0	456	4	US-09-919-039-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1  
US-09-614-679A-19  
; Sequence 19, Application US/09614679A  
; Patent No. 6492117  
; GENERAL INFORMATION:  
; APPLICANT: CHOO, YEN  
; APPLICANT: ISALAN, MARK  
; APPLICANT: PATEL, SACHIN  
; APPLICANT: BALASUBRAMANIAN, SHANKAR  
; APPLICANT: LIU, XIAOHAI  
; TITLE OF INVENTION: MOLECULES  
; FILE REFERENCE: 71278/271599  
; CURRENT APPLICATION NUMBER: US/09/614,679A  
; CURRENT FILING DATE: 2000-07-12  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-614-679A-19

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7  
Db 1 RSDHLTT 7

RESULT 2  
US-09-139-762A-19  
; Sequence 19, Application US/09139762A  
; Patent No. 6013453  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Sanchez Garcia, Isidro  
; TITLE OF INVENTION: Improvements in or Relating to  
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
; NUMBER OF SEQUENCES: 125  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Suttro, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.

```
;
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-139-762A-19

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
Db 1 RSDHLTT 7

RESULT 3
US-09-139-762A-53
; Sequence 53, Application US/09139762A
; Patent No. 6013453
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; TITLE OF INVENTION: Improvements in or Relating to
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997

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; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/040,548
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coughlin, Daniel F.
; REGISTRATION NUMBER: 36,111
; REFERENCE/DOCKET NUMBER: arcd067
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 744-0090
; TELEFAX: (312) 245-4961
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-040-548-19

Query Match 100.0%; Score 7; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
Db 1 RSDHLTT 7

RESULT 4
US-08-040-548-19
; Sequence 19, Application US/08040548
; Patent No. 5763209
; GENERAL INFORMATION:
; APPLICANT: Sukhatme, Vikas P.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
; TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5763209th Clark Street, Suite 800
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/040,548
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coughlin, Daniel F.
; REGISTRATION NUMBER: 36,111
; REFERENCE/DOCKET NUMBER: arcd067
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 744-0090
; TELEFAX: (312) 245-4961
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-040-548-19

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
Db 1 RSDHLTT 7

RESULT 4
US-08-040-548-19
; Sequence 19, Application US/08040548
; Patent No. 5763209
; GENERAL INFORMATION:
; APPLICANT: Sukhatme, Vikas P.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
; TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5763209th Clark Street, Suite 800
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/040,548
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coughlin, Daniel F.
; REGISTRATION NUMBER: 36,111
; REFERENCE/DOCKET NUMBER: arcd067
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 744-0090
; TELEFAX: (312) 245-4961
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-040-548-19

Query Match 100.0%; Score 7; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RSDHLTT 7
Db 9 RSDHLTT 15

RESULT 5
US-08-466-344-19
; Sequence 19, Application US/08466344
; Patent No. 5773583
; GENERAL INFORMATION:
; APPLICANT: Sukhacme, Vikas P.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
; TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5773583th Clark Street, Suite 800
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,344
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/040,548
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Coughlin, Daniel F.
; REGISTRATION NUMBER: 36,111
; REFERENCE/DOCKET NUMBER: arc0067
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 744-0090
; TELEFAX: (312) 245-4961
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-466-344-19

Query Match 100.0%; Score 7; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
Db 9 RSDHLTT 15

RESULT 6
US-09-229-007A-95
; Sequence 95, Application US/09229007A
; Patent No. 6453242
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Case, Casey C.
; APPLICANT: Cox III, George N.
; APPLICANT: Jamieson, Andrew
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
; TITLE OF INVENTION: to Bind to Preselcted Sites
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Imperiali, Barbara
; APPLICANT: Walkup, Grant K.
; TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:

QY 1 RSDHLTT 7
Db 8 RSDHLTT 14

RESULT 7
US-10-113-424-95
; Sequence 95, Application US/10113424
; Patent No. 6785613
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Case, Casey C.
; APPLICANT: Cox III, George N.
; APPLICANT: Jamieson, Andrew
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
; TITLE OF INVENTION: to Bind to Preselcted Sites
; FILE REFERENCE: 019496-0018000US
; CURRENT APPLICATION NUMBER: US/10/113,424
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US/09/229,007A
; PRIOR FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence
; OTHER INFORMATION: (F1, F2 and F3) from Zif 268
US-10-113-424-95

Query Match 100.0%; Score 7; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
Db 8 RSDHLTT 14

RESULT 8
US-08-620-151-111
; Sequence 111, Application US/08620151
; Patent No. 5928955
; GENERAL INFORMATION:
; APPLICANT: Imperiali, Barbara
; APPLICANT: Walkup, Grant K.
; TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:

QY 1 RSDHLTT 7
Db 8 RSDHLTT 14

RESULT 8
US-08-620-151-111
; Sequence 111, Application US/08620151
; Patent No. 5928955
; GENERAL INFORMATION:
; APPLICANT: Imperiali, Barbara
; APPLICANT: Walkup, Grant K.
; TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
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ADDRESSER: BRINKS, HOFER, GILSON & LIONE  
STREET: NBC Tower - Suite 3600, 455 N. Cityfront  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60611-5599  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,151  
FILING DATE: 22-MAR-1996  
CLASSIFICATION: 422  
ATTORNEY/AGENT INFORMATION:  
NAME: Shannon, Karen L.  
REGISTRATION NUMBER: 36,675  
REFERENCE/DOCKET NUMBER: 8597/6  
TELEPHONE: 312-321-4200  
TELEFAX: 312-321-4299  
INFORMATION FOR SEQ ID NO: 111:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-620-151-111

Query Match 100.0%; Score 7; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7  
Db 13 RSDHLTT 19

RESULT 9  
US-08-040-548-34  
Sequence 34, Application US/08040548  
Patent No. 5763209  
GENERAL INFORMATION:  
APPLICANT: Sukhatme, Vikas P.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE  
FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5763209th Clark Street, Suite 800  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/040,548  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coughlin, Daniel F.  
REGISTRATION NUMBER: 36,111  
REFERENCE/DOCKET NUMBER: arcd067  
TELEPHONE: (312) 744-0090  
TELEFAX: (312) 245-4961

INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-040-548-34

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Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLTT 7  
Db 9 RSDHLTT 15

RESULT 10  
US-08-466-344-34  
Sequence 34, Application US/08466344  
Patent No. 5773583  
GENERAL INFORMATION:  
APPLICANT: Sukhatme, Vikas P.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE  
FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5773583th Clark Street, Suite 800  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,344  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/040,548  
FILING DATE: 31-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coughlin, Daniel F.  
REGISTRATION NUMBER: 36,111  
REFERENCE/DOCKET NUMBER: arcd067  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 744-0090  
TELEFAX: (312) 245-4961  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-466-344-34

Query Match 100.0%; Score 7; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
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Qy 1 RSDHLTT 7  
Db 9 RSDHLTT 15

RESULT 11  
US-09-058-459-1

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; Sequence 1, Application US/09058459
; Patent No. 6188965
; GENERAL INFORMATION:
; APPLICANT: Mayo, Stephen L.
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Gordon, D. B.
; APPLICANT: Street, Arthur
; TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN
; FILE REFERENCE: A65353-3/RFT/RMS/SJR
; CURRENT APPLICATION NUMBER: US/09/058,459
; CURRENT FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: 60/043,464
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/054,678
; PRIOR FILING DATE: 1997-08-04
; PRIOR APPLICATION NUMBER: 60/061,097
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Mouse
; US-09-058-459-1

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Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
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Db 14 RSDHLTT 20

RESULT 12
US-09-127-926-1
; Sequence 1, Application US/09127926
; Patent No. 6269312
; GENERAL INFORMATION:
; APPLICANT: Mayo, Stephen L.
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Gordon, D. Benjamin
; APPLICANT: Street, Arthur
; APPLICANT: Su, Yaoying
; TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
; FILE REFERENCE: A65353-4/RFT/RMS/SJR
; CURRENT APPLICATION NUMBER: US/09/127,926
; CURRENT FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/043,464
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/054,678
; PRIOR FILING DATE: 1997-08-04
; PRIOR APPLICATION NUMBER: 60/061,097
; PRIOR FILING DATE: 1997-10-03
; PRIOR APPLICATION NUMBER: 09/058,459
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/087,561
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Mouse
; US-09-127-926-1

Query Match          100.0%; Score 7; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
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Db 14 RSDHLTT 20

us-09-037-179b-15
; Sequence 15, Application US/09037179B
; Patent No. 6316599
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; TITLE OF INVENTION: Wilms' Tumor Gene
; FILE REFERENCE: 0050.1312-011
; CURRENT APPLICATION NUMBER: US/09/037,179B
; CURRENT FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 08/102,942
; PRIOR FILING DATE: 1993-08-02
; PRIOR APPLICATION NUMBER: US 07/614,161
; PRIOR FILING DATE: 1990-11-13
; PRIOR APPLICATION NUMBER: US 07/435,780
; PRIOR FILING DATE: 1989-11-13
; PRIOR APPLICATION NUMBER: US 07/795,323
; PRIOR FILING DATE: 1994-09-27
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-037-179b-15

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Db 17 RSDHLTT 23

RESULT 14
US-09-240-179-2
; Sequence 2, Application US/09240179
; Patent No. 6410248
; GENERAL INFORMATION:
; APPLICANT: Greisman, Harvey A.
; APPLICANT: Pabo, Carl O.
; TITLE OF INVENTION: Massachusetts Institute of Technology
; TITLE OF INVENTION: A General Strategy for Selecting High-Affinity Zinc
; TITLE OF INVENTION: Finger Proteins for Diverse DNA Target Sites
; FILE REFERENCE: 019496-000220US
; CURRENT APPLICATION NUMBER: US/09/240,179
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: US 60/073,223
; EARLIER FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Zif268 zinc
; OTHER INFORMATION: finger 2
; US-09-240-179-2
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 13 RSDHLTT 19

RESULT 15  
US-09-714-357-1  
; Sequence 1, Application US/09714357  
; Patent No. 6708120  
; GENERAL INFORMATION:  
; APPLICANT: Mayo, Stephen L.  
; APPLICANT: Dahiyat, Bassil I.  
; APPLICANT: Gordon, D. B.  
; APPLICANT: Street, Arthur  
; TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN  
; FILE REFERENCE: A63553-3/RFT/RMS/SJR  
; CURRENT APPLICATION NUMBER: US/09/714,357  
; CURRENT FILING DATE: 2000-11-15  
; PRIOR APPLICATION NUMBER: 09/058,459  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: 60/054,678  
; PRIOR FILING DATE: 1997-08-04  
; PRIOR APPLICATION NUMBER: 60/061,097  
; PRIOR FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-714-357-1

Query Match 100.0%; Score 7; DB 4; Length 28;  
Best Local Similarity 100.0%; Pred.No. 0.043; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 14 RSDHLTT 20

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Job time : 16.8 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

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Title: US-09-846-033B-30  
Perfect score: 7  
Sequence: 1 RSDHLAR 7

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Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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2	7	100.0	100	4	US-09-248-796A-16192 Sequence 16192, A

ALIGNMENTS

RESULT 1  
US-09-779-233-42  
; Sequence 42, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
; OTHER INFORMATION: helix  
US-09-779-233-42

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RSDHLAR 7

RESULT 2

US-09-248-796A-16192  
; Sequence 16192, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 16192  
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; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-16192

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 57 RSDHLAR 63

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

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Perfect score: 7  
Sequence: 1 RSDHLAR 7

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Gapop 60.0 , Gapext 60.0

Searched: 1595201 seqs, 359116952 residues

Word size : 7

Total number of hits satisfying chosen parameters: 157

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Post-processing: Listing first 45 summaries

Database : Published Applications AA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	7	100.0	7	9 US-09-989-789-127	Sequence 127, App
3	7	100.0	7	9 US-09-989-789-202	Sequence 202, App
4	7	100.0	7	9 US-09-989-789-679	Sequence 679, App
5	7	100.0	7	9 US-09-989-789-686	Sequence 686, App
6	7	100.0	7	9 US-09-989-789-687	Sequence 687, App
7	7	100.0	7	9 US-09-989-789-893	Sequence 893, App
8	7	100.0	7	9 US-09-989-789-894	Sequence 894, App
9	7	100.0	7	9 US-09-989-789-1382	Sequence 1382, App
10	7	100.0	7	9 US-09-989-789-1388	Sequence 1388, App
11	7	100.0	7	9 US-09-989-789-1711	Sequence 1711, App
12	7	100.0	7	9 US-09-989-789-1712	Sequence 1712, App
13	7	100.0	7	9 US-09-989-789-1747	Sequence 1747, App

14	7	100.0	7	9 US-09-989-789-1748	Sequence 1748, Ap
15	7	100.0	7	9 US-09-989-789-1771	Sequence 1771, Ap
16	7	100.0	7	9 US-09-989-789-1772	Sequence 1772, Ap
17	7	100.0	7	9 US-09-989-789-1773	Sequence 1773, Ap
18	7	100.0	7	9 US-09-989-789-1775	Sequence 1775, Ap
19	7	100.0	7	9 US-09-989-789-1796	Sequence 1796, Ap
20	7	100.0	7	9 US-09-989-789-1797	Sequence 1797, Ap
21	7	100.0	7	9 US-09-989-789-2513	Sequence 2513, Ap
22	7	100.0	7	9 US-09-989-789-2534	Sequence 2534, Ap
23	7	100.0	7	9 US-09-989-789-2542	Sequence 2542, Ap
24	7	100.0	7	9 US-09-989-789-2543	Sequence 2543, Ap
25	7	100.0	7	9 US-09-989-789-2544	Sequence 2544, Ap
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27	7	100.0	7	9 US-09-989-789-2577	Sequence 2577, Ap
28	7	100.0	7	9 US-09-989-789-2580	Sequence 2580, Ap
29	7	100.0	7	9 US-09-989-789-2630	Sequence 2630, Ap
30	7	100.0	7	9 US-09-989-789-2631	Sequence 2631, Ap
31	7	100.0	7	9 US-09-989-789-2632	Sequence 2632, Ap
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36	7	100.0	7	9 US-09-989-789-2640	Sequence 2640, Ap
37	7	100.0	7	9 US-09-989-789-2641	Sequence 2641, Ap
38	7	100.0	7	9 US-09-989-789-2643	Sequence 2643, Ap
39	7	100.0	7	9 US-09-989-789-2688	Sequence 2688, Ap
40	7	100.0	7	9 US-09-989-789-2689	Sequence 2689, Ap
41	7	100.0	7	9 US-09-989-789-2710	Sequence 2710, Ap
42	7	100.0	7	9 US-09-989-789-2835	Sequence 2835, Ap
43	7	100.0	7	10 US-09-846-033B-30	Sequence 30, Appl
44	7	100.0	7	10 US-09-846-033B-34	Sequence 34, Appl
45	7	100.0	7	10 US-09-846-033B-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1  
US-09-779-233-42  
; Sequence 42, Application US/09779233  
; Patent No. US20020045158A1  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
; OTHER INFORMATION: helix  
US-09-779-233-42

Query Match 100.0%; Score 7; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLAR 7  
Db 1 RSDHLAR 7

RESULT 2  
US-09-989-789-127  
; Sequence 127, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang

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; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 127
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-127

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLAR 7
        |||||
Db      1 RSDHLAR 7

RESULT 3
US-09-989-789-202
; Sequence 202, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 202
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-202

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLAR 7
        |||||
Db      1 RSDHLAR 7

RESULT 4
US-09-989-789-679
; Sequence 679, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 679
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
```

```
US-09-989-789-679

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLAR 7
        |||||
Db      1 RSDHLAR 7

RESULT 5
US-09-989-789-686
; Sequence 686, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 686
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-686

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLAR 7
        |||||
Db      1 RSDHLAR 7

RESULT 6
US-09-989-789-687
; Sequence 687, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 687
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-687

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLAR 7
        |||||
Db      1 RSDHLAR 7

RESULT 7
US-09-989-789-893
```

```
; Sequence 893, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 893
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-893

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLAR 7
        |||||
Db      1 RSDHLAR 7

RESULT 8
US-09-989-789-894
; Sequence 894, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 894
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-894

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLAR 7
        |||||
Db      1 RSDHLAR 7

RESULT 9
US-09-989-789-1382
; Sequence 1382, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1382
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-1382

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLAR 7
        |||||
Db      1 RSDHLAR 7
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-1382

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLAR 7
        |||||
Db      1 RSDHLAR 7

RESULT 10
US-09-989-789-1388
; Sequence 1388, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1388
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-1388

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLAR 7
        |||||
Db      1 RSDHLAR 7

RESULT 11
US-09-989-789-1711
; Sequence 1711, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1711
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-1711

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLAR 7
        |||||
Db      1 RSDHLAR 7
```

```
RESULT 12
US-09-989-789-1712
; Sequence 1712, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1712
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-1712
Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLAR 7
      |||||
DB      1 RSDHLAR 7

RESULT 13
US-09-989-789-1747
; Sequence 1747, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1747
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-1747
Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLAR 7
      |||||
DB      1 RSDHLAR 7

RESULT 14
US-09-989-789-1748
; Sequence 1748, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
```

```
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1748
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-1748
```

```
Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLAR 7
      |||||
DB      1 RSDHLAR 7
```

```
RESULT 15
US-09-989-789-1771
; Sequence 1771, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1771
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-1771
```

```
Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHLAR 7
      |||||
DB      1 RSDHLAR 7
```

```
Search completed: December 27, 2004, 17:23:34
Job time : 52.45 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:30 ; Search time 66.75 Seconds  
(without alignments)  
37.620 Million cell updates/sec

Title: US-09-846-033B-30  
Perfect score: 7  
Sequence: 1 RSDHLAR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 7

Total number of hits satisfying chosen parameters: 165

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4 AAE08727	Aae08727 Human KCA
2	7	100.0	7	5 ABB80792	Abb80792 Human ER-
3	7	100.0	7	5 ABB98019	Abb98019 Zinc fing
4	7	100.0	7	5 ABB98034	Abb98034 Zinc fing
5	7	100.0	7	5 ABP49764	Abp49764 Zinc fing
6	7	100.0	7	5 ABP50067	Abp50067 Zinc fing
7	7	100.0	7	5 ABP48642	Abp48642 Zinc fing
8	7	100.0	7	5 ABP48652	Abp48652 Zinc fing
9	7	100.0	7	5 ABP49518	Abp49518 Zinc fing
10	7	100.0	7	5 ABP49797	Abp49797 Zinc fing
11	7	100.0	7	5 ABP48621	Abp48621 Zinc fing
12	7	100.0	7	5 ABP49260	Abp49260 Zinc fing
13	7	100.0	7	5 ABP50082	Abp50082 Zinc fing
14	7	100.0	7	5 ABP48649	Abp48649 Zinc fing
15	7	100.0	7	5 ABP49794	Abp49794 Zinc fing
16	7	100.0	7	5 ABP49410	Abp49410 Zinc fing
17	7	100.0	7	5 ABP49590	Abp49590 Zinc fing
18	7	100.0	7	5 ABP49515	Abp49515 Zinc fing
19	7	100.0	7	5 ABP49593	Abp49593 Zinc fing
20	7	100.0	7	5 ABP50667	Abp50667 Zinc fing
21	7	100.0	7	5 ABP49662	Abp49662 Zinc fing
22	7	100.0	7	5 ABP49902	Abp49902 Zinc fing
23	7	100.0	7	5 ABP48405	Abp48405 Zinc fing
24	7	100.0	7	5 ABP50064	Abp50064 Zinc fing
25	7	100.0	7	5 ABP50229	Abp50229 Zinc fing

26	7	100.0	7	5 ABP48216	Abp48216 Zinc fing
27	7	100.0	7	5 ABP49242	Abp49242 Zinc fing
28	7	100.0	7	5 ABP49587	Abp49587 Zinc fing
29	7	100.0	7	5 ABP49788	Abp49788 Zinc fing
30	7	100.0	7	5 ABP49791	Abp49791 Zinc fing
31	7	100.0	7	5 ABP50055	Abp50055 Zinc fing
32	7	100.0	7	5 ABP50061	Abp50061 Zinc fing
33	7	100.0	7	5 ABP50292	Abp50292 Zinc fing
34	7	100.0	7	5 ABP50058	Abp50058 Zinc fing
35	7	100.0	7	5 ABP49599	Abp49599 Zinc fing
36	7	100.0	7	5 ABP50079	Abp50079 Zinc fing
37	7	100.0	7	5 ABP49407	Abp49407 Zinc fing
38	7	100.0	7	5 ABP49701	Abp49701 Zinc fing
39	7	100.0	7	5 ABP49893	Abp49893 Zinc fing
40	7	100.0	7	5 ABP50052	Abp50052 Zinc fing
41	7	100.0	7	5 ABP48645	Abp48645 Zinc fing
42	7	100.0	7	5 ABP50085	Abp50085 Zinc fing
43	7	100.0	7	5 ABP49665	Abp49665 Zinc fing
44	7	100.0	7	5 ABP50091	Abp50091 Zinc fing
45	7	100.0	7	5 ABP50226	Abp50226 Zinc fing

ALIGNMENTS

RESULT 1  
AAE08727  
ID AAE08727 standard; peptide; 7 AA.  
AC AAE08727;  
XX  
DT 15-NOV-2001 (first entry)  
XX  
DE Human KCA4 protein F1 recognition helix.  
XX  
XX Human; KCA4; EPO; molecular target; zinc finger protein; ZFP;  
KW cellular process; signal transduction; drug-screening.  
XX  
OS Homo sapiens.  
XX  
PN WO200159450-A2.  
XX  
PD 16-AUG-2001.  
XX  
PF 08-FEB-2001; 2001WO-US004301.  
XX  
PR 08-FEB-2000; 2000US-0181117P.  
XX  
(SANG-) SANGAMO BIOSCIENCES INC.  
Case C;  
WPI; 2001-522491/57.  
XX  
PT Screening compound for interaction with molecular target by contacting  
PT compound with cells, comprising exogenous zinc finger protein that  
PT modulates expression of target, and determining values of properties of  
PT cells.  
XX  
Example 10; Page 73; 99pp; English.  
XX  
The invention relates to a method of screening a compound for interaction  
XX with a molecular target. The method involves contacting first and second  
XX cells with the compound and determining the values of properties of the  
XX compound. The second cell comprises an exogenous zinc finger protein  
XX (ZFP) that modulates the expression of the molecular target, or isolating  
XX membranes from cell comprising ZFP. The methods allow for high throughput  
XX screening of candidate compound and reduce the incidence of false  
XX positives. The methods are useful for screening a compound for  
XX interaction with a molecular target or for screening a compound for its  
XX effect on a cellular process. The method is useful for testing a compound  
XX for its capacity to transduce a signal to the molecular target or its  
XX capacity to block transduction of a signal through the molecular target,

CC and for performing biochemical drug-screening assays. The present  
 CC sequence is human KCa4 protein recognition helix used in the  
 CC exemplification of the invention

XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RSDHLAR 7  
 Db 1 RSDHLAR 7  
 |||||

RESULT 2  
 ABB80792  
 ID ABB80792 standard; peptide; 7 AA.  
 XX  
 AC ABB80792;  
 XX  
 DT 23-SEP-2002 (first entry)  
 XX  
 DE Human ER-alpha locus targeting ZFP1 peptide #2.  
 XX  
 KW ZFP; cytostatic; antidiabetic; ophthalmological; vasotropic; chromatin;  
 KW gene expression; antirheumatic; antiarthritic; antipsoriatic; neurotropic;  
 KW neuroprotective; cerebroprotective; estrogen receptor alpha; ER-alpha;  
 KW zinc finger protein.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200244386-A2.  
 XX  
 PD 06-JUN-2002.  
 XX  
 PF 30-NOV-2001; 2001WO-US045098.  
 XX  
 PR 01-DEC-2000; 2000US-0250804P.  
 XX  
 XX (SANG-) SANGAMO BIOSCIENCES INC.  
 XX  
 PI Wolffe AP, Tee C, Collingwood T;  
 XX  
 DR WPI; 2002-537455/57.  
 XX  
 PT Regulating expression of gene by contacting cell with regulatory molecule  
 PT comprising DNA-binding domain targeted to sequence within accessible  
 PT region of cellular chromatin associated with a gene, and functional  
 PT domain.  
 XX  
 PS Example 1; Page 44; 64pp; English.  
 XX

The invention relates to regulating the expression of a gene residing in  
 the chromatin of a cell. The method involves identifying one or more  
 accessible regions in cellular chromatin associated with gene; designing  
 a regulatory molecule, where the regulatory molecule comprises a DNA-  
 binding domain targeted to a sequence within the accessible region, and a  
 functional domain; and contacting the regulatory molecule with the cell.  
 The method is used for regulating the expression of a gene (e.g., a gene  
 encoding a nuclear receptor such as estrogen receptor alpha (ERalpha),  
 estrogen receptor beta (ERbeta), hepatocyte nuclear factor 4 alpha  
 (HNF4alpha), hepatocyte nuclear factor 4 gamma (HNF4gamma), peroxisome  
 proliferator activated receptor gamma (PPARGgamma), retinoid X receptor  
 alpha (RXRalpha), or constitutively active receptor alpha (CARalpha))  
 residing in the chromatin of a cell. Regulation of gene expression (such  
 as nuclear receptor genes) will be useful in treatment of various  
 diseases, including cancer, diabetes and cardiovascular disease, where  
 the regulatory molecule as described above, is contacted with the cell to  
 carry out the regulation. The method is also useful for modulation of  
 gene expression for therapeutic or prophylactic applications e.g.,  
 diabetic retinopathy, ischaemia, macular degeneration, rheumatoid  
 arthritis, psoriasis, HIV infection, sickle cell anemia, Alzheimer's

CC disease, stroke, etc. The method also has applications in pharmaceutical  
 CC research of both nuclear receptors of known function as well as those of  
 CC unknown function. The method also facilitates development of tissue and  
 CC animal models of disease states, drug validation, and therapeutic product  
 CC development. The methods also allow identification of the role of nuclear  
 CC receptors of unknown functions in cellular homeostasis. Sequences  
 CC ABB80791-817 represent zinc finger protein (ZFP) DNA-binding domains that  
 CC were fused to functional domains and tested for their ability to regulate  
 CC expression of the ER in living cells

XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RSDHLAR 7  
 Db 1 RSDHLAR 7  
 |||||

RESULT 3  
 ABB98019  
 ID ABB98019 standard; peptide; 7 AA.  
 XX  
 AC ABB98019;  
 XX  
 DT 06-SEP-2002 (first entry)  
 XX  
 DE Zinc finger protein 7 finger 1 peptide.  
 XX  
 KW Human; heparanase; cytostatic; vasotropic; antidiabetic; anti-HIV;  
 KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic;  
 KW antianemic; neuroprotective; neurotropic; cerebroprotective;  
 KW antibacterial; virucide; protozoacide; fungicide; antiinflammatory;  
 KW cardiant; immunosuppressive; tumour metastasis; inflammatory disease;  
 KW allograft rejection; cell migration; angiogenesis; basement membrane;  
 KW extracellular matrix; cancer; ischaemia; diabetic retinopathy;  
 KW macular degeneration; rheumatoid arthritis; psoriasis; HIV infection;  
 KW sickle cell anaemia; Alzheimer's disease; muscular dystrophy;  
 KW neurodegenerative disease; vascular disease; cardiovascular disease;  
 KW cystic fibrosis; stroke; gene therapy; zinc finger protein; ZFP.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200244353-A2.  
 XX  
 PD 06-JUN-2002.  
 XX  
 PF 30-NOV-2001; 2001WO-US044798.  
 XX  
 PR 30-NOV-2000; 2000US-0250690P.  
 XX  
 XX (SANG-) SANGAMO BIOSCIENCES INC.  
 XX  
 PI Wolffe AP, Qi H;  
 XX  
 DR WPI; 2002-527708/56.  
 XX  
 PT New heparanase polynucleotide, useful for controlling disease states such  
 PT as tumor metastasis, inflammatory diseases and allograft rejection.  
 XX  
 PS Example 3; Page 49; 72pp; English.  
 XX

The invention relates to novel heparanase sequences, particularly novel  
 sequences from the regulatory regions upstream and downstream of the  
 coding region. The activity of polynucleotides of the invention may be  
 described as, cytostatic, vasotropic, antidiabetic, anti-HIV,  
 CC ophthalmological, antirheumatic, antiarthritic, antipsoriatic,  
 CC antianemic, neuroprotective, neurotropic, cerebroprotective,  
 CC antibacterial, virucide, protozoacide, fungicide, antiinflammatory,  
 CC cardiant and immunosuppressive. Modulating expression of heparanase gene  
 CC using constructs of the invention is useful for facilitating targeted

CC control of disease states such as tumour metastasis, inflammatory  
 CC diseases, allograft rejection, and for inhibiting processes such as cell  
 CC migration, angiogenesis, and degradation of the basement membrane and/or  
 CC extracellular matrix. Heparanase-targeted DNA binding domains modulates  
 CC gene expression, and are useful for therapeutic or prophylactic  
 CC applications, for e.g. cancer, ischaemia, diabetic retinopathy, macular  
 CC degeneration, rheumatoid arthritis, psoriasis, HIV infection, sickle cell  
 CC anaemia, Alzheimer's disease, muscular dystrophy, neurodegenerative  
 CC diseases, vascular disease, cardiovascular disease, cystic fibrosis,  
 CC stroke, and bacterial, protozoal, fungal and viral infection. Constructs  
 CC of the invention may also be useful in gene therapy. The current sequence  
 CC represents a finger of a three-finger ZFP (zinc finger protein), which  
 CC has a target site in the human heparanase gene  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7  
 Db 1 RSDHLAR 7

RESULT 4  
 ABB98034  
 ID ABB98034 standard; peptide; 7 AA.

AC ABB98034;

DT 06-SEP-2002 (first entry)

XX Zinc finger protein 12 finger 1 peptide.

XX Human; heparanase; cytostatic; vasotropic; antidiabetic; anti-HIV;  
 KW ophthalmological; antirheumatic; antiarthritic; cerebroprotective;  
 KW antianaemic; neuroprotective; nootropic; cerebroprotective;  
 KW antibacterial; virucide; protozoacide; fungicide; antiinflammatory;  
 KW cardiant; immunosuppressive; tumour metastasis; inflammatory disease;  
 KW allograft rejection; cell migration; angiogenesis; basement membrane;  
 KW extracellular matrix; cancer; ischaemia; diabetic retinopathy;  
 KW macular degeneration; rheumatoid arthritis; psoriasis; HIV infection;  
 KW sickle cell anaemia; Alzheimer's disease; muscular dystrophy;  
 KW neurodegenerative disease; vascular disease; cardiovascular disease;  
 KW cystic fibrosis; stroke; gene therapy; zinc finger protein; ZFP.

XX Homo sapiens.

XX WO200244353-A2.

XX 06-JUN-2002.

XX 30-NOV-2001; 2001WO-US044798.

XX 30-NOV-2000; 2000US-0250690P.

XX (SANG-) SANGAMO BIOSCIENCES INC.

XX Wolffe AP, Qi H;

XX WPI; 2002-527708/56.

XX New heparanase polynucleotide, useful for controlling disease states such  
 PT as tumor metastasis, inflammatory diseases and allograft rejection.

XX Example 3; Page 49; 72pp; English.

XX The invention relates to novel heparanase sequences, particularly novel  
 CC sequences from the regulatory regions upstream and downstream of the  
 CC coding region. The activity of polynucleotides of the invention may be  
 CC described as, cytostatic, vasotropic, antidiabetic, anti-HIV,  
 CC ophthalmological, antirheumatic, antiarthritic, antipsoriatic,

CC antianaemic, neuroprotective, nootropic, cerebroprotective,  
 CC antibacterial, virucide, protozoacide, fungicide, antiinflammatory,  
 CC cardiant and immunosuppressive. Modulating expression of heparanase gene  
 CC using constructs of the invention is useful for facilitating targeted  
 CC control of disease states such as tumour metastasis, inflammatory  
 CC diseases, allograft rejection, and for inhibiting processes such as cell  
 CC migration, angiogenesis, and degradation of the basement membrane and/or  
 CC extracellular matrix. Heparanase-targeted DNA binding domains modulates  
 CC gene expression, and are useful for therapeutic or prophylactic  
 CC applications, for e.g. cancer, ischaemia, diabetic retinopathy, macular  
 CC degeneration, rheumatoid arthritis, psoriasis, HIV infection, sickle cell  
 CC anaemia, Alzheimer's disease, muscular dystrophy, neurodegenerative  
 CC diseases, vascular disease, cardiovascular disease, cystic fibrosis,  
 CC stroke, and bacterial, protozoal, fungal and viral infection. Constructs  
 CC of the invention may also be useful in gene therapy. The current sequence  
 CC represents a finger of a three-finger ZFP (zinc finger protein), which  
 CC has a target site in the human heparanase gene  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7  
 Db 1 RSDHLAR 7

RESULT 5  
 ABB49764

ID ABB49764 standard; peptide; 7 AA.

AC ABB49764;

XX 28-AUG-2002 (first entry)

XX Zinc finger protein related peptide motif SEQ ID NO:2534.

XX Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX Homo sapiens.

XX Synthetic.

XX WO200242459-A2.

XX 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US043438.

XX 20-NOV-2000; 2000US-00716637.

XX (SANG-) SANGAMO BIOSCIENCES INC.

XX Liu Q;

XX WPI; 2002-500284/53.

XX New zinc finger protein that binds to target site, useful in studying  
 PT gene function and for human therapeutics and plant engineering, comprises  
 PT first, second and third zinc fingers, ordered from N- to C-terminus.

XX Example 1; Page 54; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a  
 CC target site, comprising a first (F1), a second (F2), and a third (F3)  
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
 CC and a third (S3) target sub-site. Also described are: (i) a polypeptide  
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
 CC (3) designating (M) (I) involves selecting the F1 zinc finger such that it  
 CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it  
 CC binds to the S2 target sub-site, and selecting the F3 zinc finger such

CC that it binds to the S3 target subsite, thus designing (I) that binds to  
 CC a target site. (I) is useful for recognition of triplet target subsites  
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is  
 CC useful in studying gene function, and for human therapeutics and plant  
 CC engineering. (II), (III) or (III) is useful in therapeutic methods to  
 CC modulate the expression of a target region within a subject, in  
 CC diagnostic methods for sequence specific detection of target nucleic acid  
 CC in a sample, and in assays to determine the phenotype and function of  
 CC gene expression. (I) has improved affinity and specificity for their  
 CC target sequences, as well as enhanced biological activity. ABQ71213 to  
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
 CC finger peptides which are given in the exemplification of the present  
 CC invention.

XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 7; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7  
 Db 1 RSDHLAR 7

RESULT 6  
 ABP50067  
 ID ABP50067 standard; peptide; 7 AA.

XX AC ABP50067;  
 XX DT 28-AUG-2002 (first entry)  
 XX DE Zinc finger protein related peptide motif SEQ ID NO:2635.  
 XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN WO200242459-A2.  
 XX PD 30-MAY-2002.

XX PF 20-NOV-2001; 2001WO-US043439.  
 XX PR 20-NOV-2000; 2000US-00716637.  
 XX PA (SANG-) SANGAMO BIOSCIENCES INC.

XX PI Liu Q;

XX DR WPI; 2002-500284/53.

XX PT New zinc finger protein that binds to target site, useful in studying  
 PT gene function and for human therapeutics and plant engineering, comprises  
 PT first, second and third zinc fingers, ordered from N- to C-terminus.

XX PS Example 1; Page 56; 81pp; English.

XX CC The present invention describes a zinc finger protein (I) that binds to a  
 CC target site, comprising a first (F1), a second (F2), and a third (F3)  
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide  
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it  
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such  
 CC that it binds to the S3 target subsite, thus designing (I) that binds to  
 CC a target site. (I) is useful for recognition of triplet target subsites  
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is  
 CC useful in studying gene function, and for human therapeutics and plant

CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
 CC modulate the expression of a target region within a subject, in  
 CC diagnostic methods for sequence specific detection of target nucleic acid  
 CC in a sample, and in assays to determine the phenotype and function of  
 CC gene expression. (I) has improved affinity and specificity for their  
 CC target sequences, as well as enhanced biological activity. ABQ71213 to  
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
 CC finger peptides which are given in the exemplification of the present  
 CC invention.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7  
 Db 1 RSDHLAR 7

RESULT 7  
 ABP48642  
 ID ABP48642 standard; peptide; 7 AA.

XX AC ABP48642;

XX DT 28-AUG-2002 (first entry)

XX DE Zinc finger protein related peptide motif SEQ ID NO:696.

XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX OS Homo sapiens.  
 XX OS Synthetic.

XX PN WO200242459-A2.

XX PD 30-MAY-2002.

XX PF 20-NOV-2001; 2001WO-US043438.

XX PR 20-NOV-2000; 2000US-00716637.

XX PA (SANG-) SANGAMO BIOSCIENCES INC.

XX PI Liu Q;

XX DR WPI; 2002-500284/53.

XX PT New zinc finger protein that binds to target site, useful in studying  
 PT gene function and for human therapeutics and plant engineering, comprises  
 PT first, second and third zinc fingers, ordered from N- to C-terminus.

XX PS Example 1; Page 41; 81pp; English.

XX CC The present invention describes a zinc finger protein (I) that binds to a  
 CC target site, comprising a first (F1), a second (F2), and a third (F3)  
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide  
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it  
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such  
 CC that it binds to the S3 target subsite, thus designing (I) that binds to  
 CC a target site. (I) is useful for recognition of triplet target subsites  
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is  
 CC useful in studying gene function, and for human therapeutics and plant  
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
 CC modulate the expression of a target region within a subject, in  
 CC diagnostic methods for sequence specific detection of target nucleic acid  
 CC in a sample, and in assays to determine the phenotype and function of



CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention

XX SQ Sequence 7 AA;  
Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RSDHLAR 7  
Db 1 RSDHLAR 7  
|||||

RESULT 8  
ABP48652  
ID ABP48652 standard; peptide; 7 AA.

XX AC ABP48652;

XX DT 28-AUG-2002 (first entry)

XX Zinc finger protein related peptide motif SEQ ID NO:894.

XX Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX Homo sapiens.

XX Synthetic.

XX WO200242459-A2.

XX 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US043438.

XX 20-NOV-2000; 2000US-00716637.

XX (SANG-) SANGAMO BIOSCIENCES INC.

XX Liu Q;

XX WPI; 2002-500284/53.

XX New zinc finger protein that binds to target site, useful in studying

PT gene function and for human therapeutics and plant engineering, comprises

PT first, second and third zinc fingers, ordered from N- to C-terminus.

XX Example 1; Page 41; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a

CC target site, comprising a first (F1), a second (F2), and a third (F3)

CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the

CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),

CC and a third (S3) target sub-site. Also described are: (i) a polypeptide

CC (ii) comprising (i); (2) a polynucleotide (iii) encoding (i) or (ii); and

CC (3) designing (M) (i) involves selecting the F1 zinc finger such that it

CC binds to the S1 target sub-site, and selecting the F2 zinc finger such

CC that it binds to the S2 target sub-site, and selecting the F3 zinc finger

CC that it binds to the S3 target sub-site, thus designing (i) that binds to

CC a target site. (i) is useful for recognition of triplet target sub-sites

CC having the nucleotide G in the 5'-most position of the sub-site. (i) is

CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (i), (ii) or (iii) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determine the phenotype and function of  
CC gene expression. (i) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention

XX SQ Sequence 7 AA;  
Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RSDHLAR 7  
Db 1 RSDHLAR 7  
|||||

RESULT 9  
ABP49518  
ID ABP49518 standard; peptide; 7 AA.

XX AC ABP49518;

XX DT 28-AUG-2002 (first entry)

XX Zinc finger protein related peptide motif SEQ ID NO:1748.

XX Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX Homo sapiens.

XX Synthetic.

XX WO200242459-A2.

XX 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US043438.

XX 20-NOV-2000; 2000US-00716637.

XX (SANG-) SANGAMO BIOSCIENCES INC.

XX Liu Q;

XX WPI; 2002-500284/53.

XX New zinc finger protein that binds to target site, useful in studying

PT gene function and for human therapeutics and plant engineering, comprises

PT first, second and third zinc fingers, ordered from N- to C-terminus.

XX Example 1; Page 41; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a

CC target site, comprising a first (F1), a second (F2), and a third (F3)

CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the

CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),

CC and a third (S3) target sub-site. Also described are: (i) a polypeptide

CC (ii) comprising (i); (2) a polynucleotide (iii) encoding (i) or (ii); and

CC (3) designing (M) (i) involves selecting the F1 zinc finger such that it

CC binds to the S1 target sub-site, and selecting the F2 zinc finger such

CC that it binds to the S2 target sub-site, and selecting the F3 zinc finger

CC that it binds to the S3 target sub-site, thus designing (i) that binds to

CC a target site. (i) is useful for recognition of triplet target sub-sites

CC having the nucleotide G in the 5'-most position of the sub-site. (i) is

CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (i), (ii) or (iii) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determine the phenotype and function of  
CC gene expression. (i) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention

XX SQ Sequence 7 AA;  
Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RSDHLAR 7  
Db 1 RSDHLAR 7  
|||||

RESULT 9  
ABP49518  
ID ABP49518 standard; peptide; 7 AA.

XX AC ABP49518;

XX DT 28-AUG-2002 (first entry)

XX Zinc finger protein related peptide motif SEQ ID NO:1748.

XX Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX Homo sapiens.

XX Synthetic.

XX WO200242459-A2.

XX 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US043438.

XX 20-NOV-2000; 2000US-00716637.

XX (SANG-) SANGAMO BIOSCIENCES INC.

XX Liu Q;

XX WPI; 2002-500284/53.

XX New zinc finger protein that binds to target site, useful in studying

PT gene function and for human therapeutics and plant engineering, comprises

PT first, second and third zinc fingers, ordered from N- to C-terminus.

XX Example 1; Page 51; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a

CC target site, comprising a first (F1), a second (F2), and a third (F3)

CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the

CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),

CC and a third (S3) target sub-site. Also described are: (i) a polypeptide

CC (ii) comprising (i); (2) a polynucleotide (iii) encoding (i) or (ii); and

CC (3) designing (M) (i) involves selecting the F1 zinc finger such that it

CC binds to the S1 target sub-site, and selecting the F2 zinc finger such

CC that it binds to the S2 target sub-site, and selecting the F3 zinc finger

CC that it binds to the S3 target sub-site, thus designing (i) that binds to

CC a target site. (i) is useful for recognition of triplet target sub-sites

CC having the nucleotide G in the 5'-most position of the sub-site. (i) is

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Query Match      100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7
   |||||
Db 1 RSDHLAR 7

RESULT 10
ID ABP49797 standard; peptide; 7 AA.
XX
AC ABP49797;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related peptide motif SEQ ID NO:2545.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US043438.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS Example 1; Page 54; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subunit. Also described are: (1) a polypeptide
CC (I) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subunit, selecting the F2 zinc finger such that it
CC binds to the S2 target subunit, and selecting the F3 zinc finger such
CC that it binds to the S3 target subunit, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subunits
CC having the nucleotide G in the 5'-most position of the subunit. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
SQ Sequence 7 AA;

Query Match      100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7
   |||||
Db 1 RSDHLAR 7

RESULT 11
ID ABP48621 standard; peptide; 7 AA.
XX
AC ABP48621;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related peptide motif SEQ ID NO:679.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US043438.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS Example 1; Page 41; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subunit. Also described are: (1) a polypeptide
CC (I) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subunit, selecting the F2 zinc finger such that it
CC binds to the S2 target subunit, and selecting the F3 zinc finger such
CC that it binds to the S3 target subunit, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subunits
CC having the nucleotide G in the 5'-most position of the subunit. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
SQ Sequence 7 AA;

Query Match      100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX Zinc finger protein related peptide motif SEQ ID NO:893.
DE Zinc finger protein; ZFP, DNA binding protein; zinc finger.
KW Homo sapiens.
OS Synthetic.
PN WO200242459-A2.
XX 30-MAY-2002.
XX 20-NOV-2001; 2001WO-US043438.
XX 20-NOV-2000; 2000US-00716637.
XX (SANG-) SANGAMO BIOSCIENCES INC.
XX Liu Q;
XX WPI; 2002-500284/53.
XX New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX Example 1; Page 41; 8lpp; English.
XX The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX Sequence 7 AA;
SQ Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RSDHLAR 7
DB 1 RSDHLAR 7
RESULT 15
ABP49794
ID ABP49794 standard; peptide; 7 AA.
XX AC ABP49794;
XX DT 28-AUG-2002 (first entry)
XX DE Zinc finger protein related peptide motif SEQ ID NO:2544.
XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.

```

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XX Homo sapiens.
OS Synthetic.
XX WO200242459-A2.
XX 30-MAY-2002.
XX 20-NOV-2001; 2001WO-US043438.
XX 20-NOV-2000; 2000US-00716637.
XX (SANG-) SANGAMO BIOSCIENCES INC.
XX Liu Q;
XX WPI; 2002-500284/53.
XX New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX Example 1; Page 54; 8lpp; English.
XX The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX Sequence 7 AA;
SQ Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RSDHLAR 7
DB 1 RSDHLAR 7
Search completed: December 27, 2004, 18:06:40
Job time : 67.75 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 21:40:45 ; Search time 20 Seconds  
(without alignments)  
23.211 Million cell updates/sec

Title: US-09-846-033B-252  
Perfect score: 7  
Sequence: 1 TKDHLVR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : Issued Patents\_AA:\*
- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
------------	-------	-------------	----	-------------

No matches found

Search completed: December 27, 2004, 22:06:56  
Job time : 20.1667 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 21:40:45 ; Search time 20 Seconds  
(without alignments)  
23.211 Million cell updates/sec

Title: US-09-846-033B-251  
Perfect score: 7  
Sequence: 1 TTGHLVR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description

No matches found

Search completed: December 27, 2004, 22:06:56  
Job time : 20.1667 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 21:40:45 ; Search time 20 Seconds  
(without alignments)  
23.211 Million cell updates/sec

Title: US-09-846-033B-250  
Perfect score: 7  
Sequence: 1 TAGHLVR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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No matches found

Search completed: December 27, 2004, 22:06:56  
Job time : 20.1667 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 21:40:45 ; Search time 20 Seconds  
(without alignments)  
23.211 Million cell updates/sec

Title: US-09-846-033B-249  
Perfect score: 7  
Sequence: 1 TSGHLRR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCRUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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No matches found

Search completed: December 27, 2004, 22:06:56  
Job time : 20.1667 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 21:40:45 ; Search time 20 Seconds  
(without alignments)  
23.211 Million cell updates/sec

Title: US-09-846-033B-248  
Perfect score: 7  
Sequence: 1 TSGHLAR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	7	100.0	136	4 US-09-248-796A-19633	Sequence 19633, A
2	7	100.0	237	4 US-09-489-039A-7709	Sequence 7709, Ap

ALIGNMENTS

RESULT 1  
US-09-248-796A-19633  
; Sequence 19633, Application US/09248796A  
; Patent No. 8747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 19633  
; LENGTH: 136  
; TYPE: PRT  
; ORGANISM: Candida albicans

US-09-248-796A-19633

Query Match 100.0%; Score 7; DB 4; Length 136;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGHLAR 7  
Db 65 TSGHLAR 71

RESULT 2

US-09-489-039A-7709  
; Sequence 7709, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 7709  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-7709

Query Match 100.0%; Score 7; DB 4; Length 237;  
Best Local Similarity 100.0%; Pred. No. 0.59;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGHLAR 7  
Db 61 TSGHLAR 67

Search completed: December 27, 2004, 22:06:56  
Job time : 20.1667 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 21:40:45 ; Search time 20 Seconds  
(without alignments)  
23.211 Million cell updates/sec

Title: US-09-846-033B-247  
Perfect score: 7  
Sequence: 1 TSGHLSR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCRUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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No matches found

Search completed: December 27, 2004, 22:06:56  
Job time : 20.1667 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 Seconds  
(without alignments)  
28.393 Million cell updates/sec

Title: US-09-846-033B-108  
Perfect score: 7  
Sequence: 1 RSDALTQ 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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No matches found

Search completed: December 27, 2004, 21:40:39  
Job time : 16.35 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 Seconds  
(without alignments)  
28.393 Million cell updates/sec

Title: US-09-846-033B-107  
Perfect score: 7  
Sequence: 1 QSGNLTR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : Issued Patents AA:\*
- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfilee1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
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No matches found

Search completed: December 27, 2004, 21:40:39  
Job time : 16.35 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 Seconds  
(without alignments)  
28.393 Million cell updates/sec

Title: US-09-846-033B-106  
Perfect score: 7  
Sequence: 1 RSDHLSR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCRUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-14
2	7	100.0	7	4	US-09-779-233-44
3	7	100.0	7	4	US-09-716-637-29
4	7	100.0	99	4	US-09-229-037-15
5	7	100.0	99	4	US-09-478-681-15
6	7	100.0	99	4	US-09-779-233-3
7	7	100.0	196	4	US-09-229-037-30
8	7	100.0	196	4	US-09-478-681-30
9	7	100.0	196	4	US-09-779-233-18

ALIGNMENTS

RESULT 1  
US-09-731-558-14  
; Sequence 14, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558

; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SBS3  
; OTHER INFORMATION: recognition helix  
US-09-731-558-14

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
| | | | |  
Db 1 RSDHLSR 7

RESULT 2

US-09-779-233-44  
; Sequence 44, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
; OTHER INFORMATION: helix  
US-09-779-233-44

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
| | | | |  
Db 1 RSDHLSR 7

RESULT 3

US-09-716-637-29  
; Sequence 29, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29

Query Match      100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 1 RSDHLSR 7

RESULT 4
US-09-229-037-15
; Sequence 15, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP
; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-229-037-15

Query Match      100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 5
US-09-478-681-15
; Sequence 15, Application US/09478681
; Patent No. 6607882
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric E.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS
; FILE REFERENCE: 8325-0002.10 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/478,681
; CURRENT FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP
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; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-478-681-15

Query Match      100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 6
US-09-779-233-3
; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3

Query Match      100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 7
US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-229-037-30

Query Match      100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RSDHLSR 7  
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Db 178 RSDHLSR 184

RESULT 8  
US-09-478-681-30  
; Sequence 30, Application US/09478681  
; Patent No. 6607882  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:designed  
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpni to BamHI  
US-09-478-681-30

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
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Db 178 RSDHLSR 184

RESULT 9  
US-09-779-233-18  
; Sequence 18, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1  
US-09-779-233-18

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
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Db 178 RSDHLSR 184

Search completed: December 27, 2004, 21:40:39  
Job time : 17.35 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 Seconds  
(without alignments)  
28.393 Million cell updates/sec

Title: US-09-846-033B-105  
Perfect score: 7  
Sequence: 1 RSDHLSR 7

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Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*

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- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	7	100.0	7	4	US-09-779-233-44
3	7	100.0	7	4	US-09-716-637-29
4	7	100.0	99	4	US-09-229-037-15
5	7	100.0	99	4	US-09-478-681-15
6	7	100.0	99	4	US-09-779-233-3
7	7	100.0	196	4	US-09-229-037-30
8	7	100.0	196	4	US-09-478-681-30
9	7	100.0	196	4	US-09-779-233-18

ALIGNMENTS

RESULT 1  
US-09-731-558-14  
; Sequence 14, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558

; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:SBS3  
; OTHER INFORMATION: recognition helix  
US-09-731-558-14

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
| | | | |  
Db 1 RSDHLSR 7

RESULT 2

US-09-779-233-44  
; Sequence 44, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
; OTHER INFORMATION: helix  
US-09-779-233-44

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
| | | | |  
Db 1 RSDHLSR 7

RESULT 3

US-09-716-637-29  
; Sequence 29, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29

Query Match          100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 1 RSDHLSR 7

RESULT 4
US-09-229-037-15
; Sequence 15, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-229-037-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 5
US-09-478-681-15
; Sequence 15, Application US/09478681
; Patent No. 6607882
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric E.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS
; FILE REFERENCE: 8325-0002.10 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/478,681
; CURRENT FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
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; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-478-681-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 6
US-09-779-233-3
; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 7
US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-229-037-30

Query Match          100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RSDHLSR 7  
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Db 178 RSDHLSR 184

RESULT 8  
US-09-478-681-30  
; Sequence 30, Application US/09478681  
; Patent No. 6607882  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:designed  
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpni to BamHI  
US-09-478-681-30

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSR 7  
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Db 178 RSDHLSR 184

RESULT 9  
US-09-779-233-18  
; Sequence 18, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1  
US-09-779-233-18

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSR 7  
|||||||  
Db 178 RSDHLSR 184

Search completed: December 27, 2004, 21:40:38  
Job time : 16.35 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 Seconds  
(without alignments)  
28.393 Million cell updates/sec

Title: US-09-846-033b-104  
Perfect score: 7  
Sequence: 1 RSDHLSR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	7	100.0	7	4 US-09-779-233-44	Sequence 44, Appl
3	7	100.0	7	4 US-09-716-637-29	Sequence 29, Appl
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5	7	100.0	99	4 US-09-478-681-15	Sequence 15, Appl
6	7	100.0	99	4 US-09-779-233-3	Sequence 3, Appl
7	7	100.0	196	4 US-09-229-037-30	Sequence 30, Appl
8	7	100.0	196	4 US-09-478-681-30	Sequence 30, Appl
9	7	100.0	196	4 US-09-779-233-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1  
US-09-731-558-14  
; Sequence 14, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558

; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SBS3  
; OTHER INFORMATION: recognition helix  
; US-09-731-558-14

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
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Db 1 RSDHLSR 7

RESULT 2

US-09-779-233-44  
; Sequence 44, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
; OTHER INFORMATION: helix  
; US-09-779-233-44

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
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Db 1 RSDHLSR 7

RESULT 3

US-09-716-637-29  
; Sequence 29, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29

Query Match      100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
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Db 1 RSDHLSR 7

RESULT 4
US-09-229-037-15
; Sequence 15, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-229-037-15

Query Match      100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
   |||||
Db 81 RSDHLSR 87

RESULT 5
US-09-478-681-15
; Sequence 15, Application US/09478681
; Patent No. 6607882
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric E.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS
; FILE REFERENCE: 8325-0002.10 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/478,681
; CURRENT FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-229-037-15

Query Match      100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
   |||||
Db 81 RSDHLSR 87

RESULT 6
US-09-779-233-3
; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3

Query Match      100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
   |||||
Db 81 RSDHLSR 87

RESULT 7
US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpni to BamHI
US-09-229-037-30

Query Match      100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RSDHLSR 7  
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Db 178 RSDHLSR 184

RESULT 8  
US-09-478-681-30  
; Sequence 30, Application US/09478681  
; Patent No. 6607882  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:designed  
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpni to BamHI  
US-09-478-681-30

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSR 7  
|||||  
Db 178 RSDHLSR 184

RESULT 9  
US-09-779-233-18  
; Sequence 18, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Casey, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1  
US-09-779-233-18

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSR 7  
|||||  
Db 178 RSDHLSR 184

Search completed: December 27, 2004, 21:40:38  
Job time : 16.35 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 Seconds  
(without alignments)  
28.393 Million cell updates/sec

Title: US-09-846-033B-103  
Perfect score: 7  
Sequence: 1 RSDHLSR 7

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Searched: 478139 seqs, 66318000 residues

Word size : 7

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Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-14
2	7	100.0	7	4	US-09-779-233-44
3	7	100.0	7	4	US-09-716-637-29
4	7	100.0	99	4	US-09-229-037-15
5	7	100.0	99	4	US-09-478-681-15
6	7	100.0	99	4	US-09-779-233-3
7	7	100.0	196	4	US-09-229-037-30
8	7	100.0	196	4	US-09-478-681-30
9	7	100.0	196	4	US-09-779-233-18

ALIGNMENTS

RESULT 1  
US-09-731-558-14  
; Sequence 14, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Casey, Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558

; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:SBS3  
; OTHER INFORMATION: recognition helix  
US-09-731-558-14

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
Db 1 RSDHLSR 7

RESULT 2

US-09-779-233-44  
; Sequence 44, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Casey, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
; OTHER INFORMATION: helix  
US-09-779-233-44

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
Db 1 RSDHLSR 7

RESULT 3

US-09-716-637-29  
; Sequence 29, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29

Query Match          100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
DB 1 RSDHLSR 7

RESULT 4
US-09-229-037-15
; Sequence 15, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; FILE REFERENCE: 8325-00210 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-229-037-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
DB 81 RSDHLSR 87

RESULT 5
US-09-478-681-15
; Sequence 15, Application US/09478681
; Patent No. 6607882
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric E.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; FILE REFERENCE: 8325-0002.10 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/478,681
; CURRENT FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
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;
; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-478-681-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
DB 81 RSDHLSR 87

RESULT 6
US-09-779-233-3
; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
DB 81 RSDHLSR 87

RESULT 7
US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-229-037-30

Query Match          100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RSDHLSR 7  
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Db 178 RSDHLSR 184

RESULT 8  
US-09-478-681-30  
; Sequence 30, Application US/09478681  
; Patent No. 6607882  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:designed  
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI  
US-09-478-681-30

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
|||||  
Db 178 RSDHLSR 184

RESULT 9  
US-09-779-233-18  
; Sequence 18, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1  
US-09-779-233-18

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
|||||  
Db 178 RSDHLSR 184

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 Seconds  
(without alignments)  
28.393 Million cell updates/sec

Title: US-09-846-033b-102

Perfect score: 7  
Sequence: 1 RSDHLSR 7

Scoring table: OLIGO  
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Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4 US-09-731-558-14	Sequence 14, Appl
2	7	100.0	7	4 US-09-779-233-44	Sequence 44, Appl
3	7	100.0	7	4 US-09-716-637-29	Sequence 29, Appl
4	7	100.0	99	4 US-09-229-037-15	Sequence 15, Appl
5	7	100.0	99	4 US-09-478-681-15	Sequence 15, Appl
6	7	100.0	99	4 US-09-779-233-3	Sequence 3, Appl
7	7	100.0	196	4 US-09-229-037-30	Sequence 30, Appl
8	7	100.0	196	4 US-09-478-681-30	Sequence 30, Appl
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#### ALIGNMENTS

RESULT 1  
US-09-731-558-14  
; Sequence 14, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558

; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:SSS3  
; OTHER INFORMATION: recognition helix  
US-09-731-558-14

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
DB 1 RSDHLSR 7

#### RESULT 2

US-09-779-233-44  
; Sequence 44, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
; OTHER INFORMATION: helix  
US-09-779-233-44

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
DB 1 RSDHLSR 7

#### RESULT 3

US-09-716-637-29  
; Sequence 29, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29

Query Match          100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 1 RSDHLSR 7

RESULT 4
US-09-229-037-15
; Sequence 15, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-229-037-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 5
US-09-478-681-15
; Sequence 15, Application US/09478681
; Patent No. 6607882
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric E.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS
; FILE REFERENCE: 8325-0002.10 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/478,681
; CURRENT FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
```

```
; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-478-681-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 6
US-09-779-233-3
; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 7
US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-229-037-30

Query Match          100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RSDHLSR 7  
|||||||  
Db 178 RSDHLSR 184

RESULT 8  
US-09-478-681-30  
; Sequence 30, Application US/09478681  
; Patent No. 6607882  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:designed  
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpnl to BamHI  
US-09-478-681-30

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSR 7  
|||||||  
Db 178 RSDHLSR 184

RESULT 9  
US-09-779-233-18  
; Sequence 18, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1  
US-09-779-233-18

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSR 7  
|||||||  
Db 178 RSDHLSR 184

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OM protein - protein search, using sw model

Run on: December 27, 2004, 20:25:55 ; Search time 64.3 Seconds  
(without alignments)  
39.053 Million cell updates/sec

Title: US-09-846-033B-246  
Perfect score: 7  
Sequence: 1 TSGHLIR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 7

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	5 ABJ03961	Abj03961 Human VEG
2	7	100.0	7	6 ABO14621	Abol4621 Human VEG

ALIGNMENTS

RESULT 1  
ABJ03961  
ID ABJ03961 standard; peptide; 7 AA.  
XX  
AC ABJ03961;  
XX  
DT 25-SEP-2002 (first entry)  
XX  
DE Human VEGF-targeted zinc finger protein fragment SEQ ID NO: 246.  
XX  
KW Zinc finger protein; angiogenesis; vasculogenesis; ischaemia;  
KW diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth;  
KW gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnery;  
KW antitumor; cytostatic; antipsoriatic; antidiabetic; ophthalmological;  
KW osteopathic; antiinfertility.  
XX  
OS Homo sapiens.  
XX

PN WO200246412-A2.  
XX  
PD 13-JUN-2002.  
XX  
PF 06-DEC-2001; 2001WO-US046861.  
XX  
PR 07-DEC-2000; 2000US-00733604.  
PR 12-DEC-2000; 2000US-00736083.  
PR 30-APR-2001; 2001US-00846033.  
XX  
PA (SANG-) SANGAMO BIOSCIENCES INC.  
XX  
PI Rebar E, Jamieson A, Liu Q, Liu P, Wolffe A, Eisenberg SP;  
PI Jarvis E;  
XX  
DR WPI; 2002-527918/56.  
XX  
PT New zinc finger protein that binds to target site in vascular endothelial  
PT growth factor gene, useful for modulating expression of the gene and for  
PT treating atherosclerosis, ischemia, arthritis, wound or ulcer.  
XX  
PS Claim 4; Page 103; 195pp; English.  
XX  
CC The present invention relates to a zinc finger protein that binds to a  
CC target site in one or more vascular endothelial growth factor (VEGF)  
CC genes. The protein is useful for modulating expression of a VEGF gene,  
CC thereby regulating angiogenesis and vasculogenesis. This can be used to  
CC treat atherosclerosis, ischaemia, arthritis, wounds, ulcers, tumours,  
CC diabetic retinopathy or psoriasis. The present sequence is a peptide  
CC shown in the invention  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0;  
QY 1 TSGHLIR 7  
DB 1 TSGHLIR 7  
RESULT 2  
ABO14621  
ID ABO14621 standard; peptide; 7 AA.  
XX  
AC ABO14621;  
XX  
DT 22-AUG-2003 (first entry)  
XX  
DE Human VEGF-targeted ZFP VOP 32-D recognition helix F2.  
XX  
KW Zinc finger protein; vascular endothelial growth factor; VEGF; ischaemia;  
KW atherosclerosis; tumour; arthritis; bone injury; wound; ulcer; surgery;  
KW angiogenesis; pregnancy; embryogenesis; human; recognition helix.  
XX  
OS Homo sapiens.  
XX  
PN US2003021776-A1.  
XX  
PD 30-JAN-2003.  
XX  
PF 06-DEC-2001; 2001US-00006069.  
XX  
PR 07-DEC-2000; 2000US-00733604.  
PR 12-DEC-2000; 2000US-00736083.  
PR 30-APR-2001; 2001US-00846033.  
XX  
PA (SANG-) SANGAMO BIOSCIENCES INC.  
XX  
PI Rebar E, Jamieson A, Liu Q, Liu P, Wolffe A, Eisenberg SP;  
PI Jarvis E;  
XX

DR WPI; 2003-466074/44.  
 XX  
 PT Novel zinc finger protein that binds to a target site, useful for  
 PT modulating vascular endothelial growth factor gene expression, for  
 PT modulating angiogenesis, for wound healing and for treating ischemia.  
 XX  
 PS Disclosure; Page 43; 120pp; English.  
 XX  
 CC The invention relates to a zinc finger protein that binds to a target  
 CC site. The zinc finger protein is useful for modulating expression of a  
 CC vascular endothelial growth factor (VEGF) gene. The expression of a  
 CC number of splice variants of VEGF gene is modulated. A number of target  
 CC sites are contacted with a number of zinc finger proteins and each zinc  
 CC finger protein binds to a distinct target site. The zinc finger protein  
 CC is administered in combination with a delivery vehicle, or its nucleic  
 CC acid is administered into the cell, either in naked form or delivered in  
 CC an expression vector. The zinc finger protein or nucleic acid is useful  
 CC for treating a disease or injury such as atherosclerosis, ischaemia,  
 CC tumour, arthritis, bone injury, wounds and ulcer in a subject. The zinc  
 CC finger protein is also useful for modulating angiogenesis, by introducing  
 CC the zinc finger protein into an animal, where the animal has a genome  
 CC comprising a target site within a VEGF gene. The zinc finger protein is  
 CC also useful for screening for a modulator of expression of a VEGF gene.  
 CC The zinc finger protein and nucleic acid are also useful to promote  
 CC development of the corpus luteum and endometrium, which is useful for  
 CC initiating and/or maintaining pregnancy and for supporting embryogenesis.  
 CC The zinc finger protein and its nucleic acid are also useful in surgical  
 CC applications. The present sequence represents the amino acid sequence of  
 CC a human VEGF targeted zinc finger protein ZFP recognition helix  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 6; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TSGHLIR 7  
 Db 1 TSGHLIR 7

Search completed: December 27, 2004, 21:35:10  
 Job time : 64.3 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 Seconds  
(without alignments)  
28.393 Million cell updates/sec

Title: US-09-846-033B-246  
Perfect score: 7  
Sequence: 1 TSGHLIR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents\_AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
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No matches found

Search completed: December 27, 2004, 21:40:40  
Job time : 16.35 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 Seconds  
(without alignments)  
28.393 Million cell updates/sec

Title: US-09-846-033B-245  
Perfect score: 7  
Sequence: 1 TSGHLTR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents\_AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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No matches found

Search completed: December 27, 2004, 21:40:40  
Job time : 16.35 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 Seconds  
(without alignments)  
28.393 Million cell updates/sec

Title: US-09-846-033B-115  
Perfect score: 7  
Sequence: 1 QSSDLTR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	4	US-09-731-558-17
2	7	100.0	7	4	US-09-779-233-37

ALIGNMENTS

RESULT 1  
US-09-731-558-17  
; Sequence 17, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558  
; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 7

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SBS6  
; OTHER INFORMATION: recognition helix  
US-09-731-558-17

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSDLTR 7  
| | | | |  
Db 1 QSSDLTR 7

RESULT 2

US-09-779-233-37  
; Sequence 37, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: linker  
US-09-779-233-37

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSDLTR 7  
| | | | |  
Db 1 QSSDLTR 7

Search completed: December 27, 2004, 21:40:40  
Job time : 16.35 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 Seconds  
(without alignments)  
28.393 Million cell updates/sec

Title: US-09-846-033B-114  
Perfect score: 7  
Sequence: 1 RSDHLSR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-14
2	7	100.0	7	4	US-09-779-233-44
3	7	100.0	7	4	US-09-716-637-29
4	7	100.0	99	4	US-09-229-037-15
5	7	100.0	99	4	US-09-478-681-15
6	7	100.0	99	4	US-09-779-233-3
7	7	100.0	196	4	US-09-229-037-30
8	7	100.0	196	4	US-09-478-681-30
9	7	100.0	196	4	US-09-779-233-18

ALIGNMENTS

RESULT 1  
US-09-731-558-14  
; Sequence 14, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731.558

; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SRS3  
; OTHER INFORMATION: recognition helix  
US-09-731-558-14

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
Db 1 RSDHLSR 7

RESULT 2

US-09-779-233-44  
; Sequence 44, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
; OTHER INFORMATION: helix  
US-09-779-233-44

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
Db 1 RSDHLSR 7

RESULT 3

US-09-716-637-29  
; Sequence 29, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang  
; APPLICANT: JAMIESON, Andrew  
; APPLICANT: REBAR, Edward  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29

Query Match          100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSR 7
Db 1 RSDHLSR 7

RESULT 4
US-09-229-037-15
; Sequence 15, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-229-037-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 5
US-09-478-681-15
; Sequence 15, Application US/09478681
; Patent No. 6607882
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric E.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS
; FILE REFERENCE: 8325-0002.10 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/478,681
; CURRENT FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
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; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-478-681-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 6
US-09-779-233-3
; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 7
US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-229-037-30

Query Match          100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RSDHLSR 7  
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Db 178 RSDHLSR 184

RESULT 8  
US-09-478-681-30  
; Sequence 30, Application US/09478681  
; Patent No. 6607882  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:designed  
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpni to BamHI  
US-09-478-681-30

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
|||||  
Db 178 RSDHLSR 184

RESULT 9  
US-09-779-233-18  
; Sequence 18, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1  
US-09-779-233-18

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
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Db 178 RSDHLSR 184

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Job time : 16.35 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 Seconds  
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28.393 Million cell updates/sec

Title: US-09-846-033B-113  
Sequence: 1 RSDHLSR 7

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Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

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Total number of hits satisfying chosen parameters: 9

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	7	100.0	7	4	US-09-731-558-14
2	7	100.0	7	4	US-09-779-233-44
3	7	100.0	7	4	US-09-716-637-29
4	7	100.0	99	4	US-09-229-037-15
5	7	100.0	99	4	US-09-478-681-15
6	7	100.0	99	4	US-09-779-233-3
7	7	100.0	196	4	US-09-229-037-30
8	7	100.0	196	4	US-09-478-681-30
9	7	100.0	196	4	US-09-779-233-18

ALIGNMENTS

RESULT 1  
US-09-731-558-14  
; Sequence 14, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558

; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:SBS3  
; OTHER INFORMATION: recognition helix  
US-09-731-558-14

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
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Db 1 RSDHLSR 7

RESULT 2

US-09-779-233-44  
; Sequence 44, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
; OTHER INFORMATION: helix  
US-09-779-233-44

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
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Db 1 RSDHLSR 7

RESULT 3

US-09-716-637-29  
; Sequence 29, Application US/09716637  
; Patent No. 6794136  
; GENERAL INFORMATION:  
; APPLICANT: EISENBERG, Stephen P.  
; APPLICANT: LIU, Qiang Andrew  
; APPLICANT: REBAR, Edward  
; APPLICANT: JAMIESON, Andrew  
; TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 8325-0020  
; CURRENT APPLICATION NUMBER: US/09/716,637  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I P3
US-09-716-637-29

Query Match          100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 1 RSDHLSR 7

RESULT 4
US-09-229-037-15
; Sequence 15, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Spratt, Sharon Kaye
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
; OTHER INFORMATION: construct targeting upstream 9-base pair target
; OTHER INFORMATION: site in VEGF promoter
US-09-229-037-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 5
US-09-478-681-15
; Sequence 15, Application US/09478681
; Patent No. 6607882
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric E.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS
; FILE REFERENCE: 8325-0002.10 / S2-US3
; CURRENT APPLICATION NUMBER: US/09/478,681
; CURRENT FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
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;
; OTHER INFORMATION: construct targeting upstream 9-base pair target
US-09-478-681-15

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 6
US-09-779-233-3
; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3

Query Match          100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7
Db 81 RSDHLSR 87

RESULT 7
US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox III, George No. 6534261bert
; APPLICANT: Case, Casey Christopher
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric Edward
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-002200US
; CURRENT APPLICATION NUMBER: US/09/229,037A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-229-037-30

Query Match          100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RSDHLSR 7  
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Db 178 RSDHLSR 184

RESULT 8  
US-09-478-681-30  
; Sequence 30, Application US/09478681  
; Patent No. 6607882  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Case, Casey Christopher  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric E.  
; APPLICANT: Spratt, Sharon K.  
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS  
; TITLE OF INVENTION: USING ZINC FINGER PROTEINS  
; FILE REFERENCE: 8325-0002.10 / S2-US3  
; CURRENT APPLICATION NUMBER: US/09/478,681  
; CURRENT FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:designed  
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from Kpni to BamHI  
US-09-478-681-30

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
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Db 178 RSDHLSR 184

RESULT 9  
US-09-779-233-18  
; Sequence 18, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1  
US-09-779-233-18

Query Match 100.0%; Score 7; DB 4; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLSR 7  
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Db 178 RSDHLSR 184

Search completed: December 27, 2004, 21:40:40  
Job time : 17.35 secs

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